



#3

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<110> Benjanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US5.DIV

<140> US 09/992,095

<141> 2001-11-13

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<151> 2001-08-06

<150> PCT/IB01/01715

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<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<160> 112

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cgttgccaca	gttttgatga	tc	atctctct	cccaaccaag	atggtggaaa	aagcaaaaac	180
gtggtgaatc	ttggagcaat	ccgacaaggc	atgaaacgct	tccaatttct	gttaaactgc		240
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Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser Thr
20 25 30
gac cac acc aaa atg cca tct caa atg gaa cac gcc atg gaa acc atg 1581
Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met
35 40 45
atg ttt aca ttt cac aaa ttc gct ggg gat aaa ggc tac tta aca aag 1629
Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr Lys
50 55 60 65
gag gac ctg aga gta ctc atg gaa aag gag ttc cct gga ttt ttg gaa 1677
Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu Glu
70 75 80
aat caa aaa gac cct ctg gct gtg gac aaa ata atg aag gac ctg gac 1725
Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp
85 90 95
cag tgt aga gat ggc aaa gtg ggc ttc cag agc ttc ttt tcc cta att 1773
Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu Ile
100 105 110
gcg ggc ctc acc att gca tgc aat gac tat ttt gta gta cac atg aag 1821
Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys
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Gln Lys Gly Lys Lys
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 35 40 45
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 Lys Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu
 65 70 75 80
 Glu Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu
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 Asp Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu
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 ctg aac gca gga gct gtc att gac tgg ccc aca gag gag ggc aag gaa 152
 Leu Asn Ala Gly Ala Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu
 1 5 10
 gta tgg gat tat gtg acg gtc cgc aag gat gcc tac atg ttc tgg tgg 200
 Val Trp Asp Tyr Val Thr Val Arg Lys Asp Ala Tyr Met Phe Trp Trp
 15 20 25
 ctc tat tat gcc acc aac tcc tgc aag aac ttc tca gaa ctg ccc ctg 248
 Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu
 30 35 40 45

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Val Met Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly	
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aac ttt gag gaa att ggg ccc ctt gac agt gat ctc aaa cca cgg aaa	344
Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys	
65 70 75	
acc acc tgg ctc cag gct gcc agt ctc cta ttt gtg gat aat ccc gtg	392
Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val	
80 85 90	
ggc act ggg ttc agt tat gtg aat ggt agt ggt gcc tat gcc aag gac	440
Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp	
95 100 105	
ctg gct atg gtg gct tca gac atg atg gtt ctc ctg aag acc ttc ttc	488
Leu Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe	
110 115 120 125	
agt tgc cac aaa gaa ttc cag aca gtt cca ttc tac att ttc tca gag	536
Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu	
130 135 140	
tcc tat gga gga aaa atg gca gct ggc att ggt cta gag ctt tat aag	584
Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys	
145 150 155	
gcc att cag cga ggg acc atc aag tgc aac ttt gcg ggg gtt gcc ttg	632
Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu	
160 165 170	
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Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro	
175 180 185	
tac ctg tac agc atg tct ctt ctc gaa gac aaa ggt ctg gca gag gtg	728
Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys Gly Leu Ala Glu Val	
190 195 200 205	
tct aag gtt gca gag caa gta ctg aat gcc gta aat aag ggg ctc tac	776
Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr	
210 215 220	
aga gag gcc aca gag ctg tgg ggg aaa gca gaa atg atc att gaa cag	824
Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln	
225 230 235	
gta aaa agg gga aac act cag agg cta gcc tgc ttg gct ttt tct ggt	872
Val Lys Arg Gly Asn Thr Gln Arg Leu Ala Cys Leu Ala Phe Ser Gly	
240 245 250	
ggg tac agg gcc cat ggt tgg tgt tgt caa act tgg agt cta cac	917
Gly Tyr Arg Ala His Gly Trp Cys Cys Gln Thr Trp Ser Leu His	
255 260 265	
tgaggctccc cacatatctg caaatgattg catgctggat aataaatctc ttgggtctaa	977
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Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	Ser	Cys	Lys	Asn	
		25					30					35				
Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	Gly	Gly	Pro	Gly	Gly	
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Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	Ile	Gly	Pro	Leu	Asp	Ser	
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Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	Leu	Gln	Ala	Ala	Ser	Leu	Leu	
				75				80						85		
Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	
			90				95						100			
Gly	Ala	Tyr	Ala	Lys	Asp	Leu	Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	
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Leu	Leu	Lys	Thr	Phe	Phe	Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	
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Phe	Tyr	Ile	Phe	Ser	Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	
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Phe	Ala	Gly	Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	
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Val	Leu	Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	
	185					190						195				
Lys	Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	
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Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	Ala	
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Glu	Met	Ile	Ile	Glu	Gln	Val	Lys	Arg	Gly	Asn	Thr	Gln	Arg	Leu	Ala	
			235					240						245		
Cys	Leu	Ala	Phe	Ser	Gly	Gly	Tyr	Arg	Ala	His	Gly	Trp	Cys	Cys	Gln	
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                               -15                               -10
gct ctc atg att tcc atg att agc gct gat tca cat gaa aag aga cat 161
Ala Leu Met Ile Ser Met Ile Ser Ala Asp Ser His Glu Lys Arg His
                               -5                               1                               5
cat ggg tat aga aga aaa ttc cat gaa aag cat cat tca tac cat atc 209
His Gly Tyr Arg Arg Lys Phe His Glu Lys His His Ser Tyr His Ile
                               10                               15                               20
aca cta cta cca ctt ttt gaa gaa tca tca aag agc aat gca aat gaa 257
Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu
25                               30                               35                               40
aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305
Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe
                               45                               50                               55
tca att gtc act tgatgatata attgcaattt aaactgttaa gctgtgttca 357
Ser Ile Val Thr
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Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
15                               20                               25
Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu Lys His Tyr Asn Leu Leu
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 Leu Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
 -10 -5 1
 atg act cag tct cca ctc ttc ctg ccc gtc acc cct gga gag ccg gcc 148
 Met Thr Gln Ser Pro Leu Phe Leu Pro Val Thr Pro Gly Glu Pro Ala
 5 10 15 20
 tcc atc tcc tgc agg tct agt cag agc ctc ctg cat gtt caa ggg tcc 196
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu His Val Gln Gly Ser
 25 30 35
 aac tat ttg gat tgg tac cac cag aag cca ggg cag tct cca caa ctc 244
 Asn Tyr Leu Asp Trp Tyr His Gln Lys Pro Gly Gln Ser Pro Gln Leu
 40 45 50
 ctg ata tac ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc 292
 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
 55 60 65
 agt ggc agt gga tca ggc aca gat ttc aca ctg aaa atc agt aga gtg 340
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 70 75 80
 gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct cta caa act 388
 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
 85 90 95 100
 cca ttc act ttc ggc cct ggg acc aga gtg gat atc aag cga act gtg 436
 Pro Phe Thr Phe Gly Pro Gly Thr Arg Val Asp Ile Lys Arg Thr Val
 105 110 115
 gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 484
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 120 125 130
 tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 532
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 135 140 145
 gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 580
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 150 155 160
 tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 628
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175 180
 ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 676
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 185 190 195
 gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 724
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
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Lys Ser Phe Asn Arg Gly Glu Cys

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      215                      220
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Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
15 20 25
Leu Leu His Val Gln Gly Ser Asn Tyr Leu Asp Trp Tyr His Gln Lys
30 35 40
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
45 50 55 60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
65 70 75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90
Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly Pro Gly Thr Arg
95 100 105
Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110 115 120
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135 140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185
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Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

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gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
gccctcaggc ctcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
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Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
1 5 10 15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
20 25 30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
35 40 45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
50 55 60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
65 70 75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
80 85 90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggttatcagc 634
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20 25 30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35 40 45 50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
55 60 65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
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85

90

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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccct 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694
 aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

<210> 12
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

<400> 12

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<210> 14
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 <212> PRT
 <213> Homo sapiens

<220>
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 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

<210> 15
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 <212> DNA
 <213> Homo sapiens

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<220>
 <221> 3'UTR
 <222> 575..733

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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccct 240
 tctgcctagg agc atg tct gcc tcc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30


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ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
      35      40      45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
      50      55      60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65      70      75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80      85      90
tgagccctga gctaattaag tgctggataa gcatacctc ccagtaatcc tggtatcagc 634
ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcaggtg 694
aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

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<210> 16
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

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Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
      5      10      15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20      25      30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35      40      45      50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
      55      60      65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
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Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      85      90

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<210> 17
 <211> 1175
 <212> DNA
 <213> Homo sapiens

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 <222> 327..1013

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 <221> 3'UTR
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<221> polyA_signal

<222> 1131..1136

<220>

<221> polyA_site

<222> 1160..1175

<400> 17

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taggactttt cccatccaat tttgtaacaa ctaatttaaa catagagact gaggcagcgg 240
ctgtggacaa attgaatgta attgatgatg atgtggagga aattaagaaa tcagagcctg 300
agcctgttta tatagatgag gataag atg gat aga gcc ctg cag gta ctt cag 353
                               Met Asp Arg Ala Leu Gln Val Leu Gln
                               1 5
agt ata gat cca aca gat tca aaa cca gac tcc caa gac ctt ttg gat 401
Ser Ile Asp Pro Thr Asp Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp
10 15 20 25
tta gaa gat atc tgc caa cag atg ggt cca atg ata gat gaa aaa ctt 449
Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu
30 35 40
gaa gaa att gat agg aag cat tca gaa ttg tct gaa ttg aat gtt aaa 497
Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys
45 50 55
gtc ctg gaa gct ctg gaa cta tat aac aaa ttg gtg aat gaa gca cca 545
Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro
60 65 70
gtg tac tca gtc tat tca aag ctc cac cct cca gca cat tac cca cct 593
Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro
75 80 85
gca tca tct ggg gtt cca atg cag aca tat cca gtt caa tca cat ggt 641
Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly
90 95 100 105
gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc 689
Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser
110 115 120
tat agc cta gga ccc gat caa att ggt cca ctg aga tct ctg cct cca 737
Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro
125 130 135
aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta 785
Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu
140 145 150
agc act gga caa gac act gtt tcc aat cct act tat atg aac cag aac 833
Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn
155 160 165
tct aac cta cag tca gct act ggt aca act gct tac aca cag caa atg 881
Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met
170 175 180 185
ggg atg tct gtg gat atg tca tct tat cag aac act act tcc aat ttg 929
Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu
190 195 200
cct caa ctg gca ggc ttt ccg gtg aca gtt cca gct cat cca gtt gca 977
Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala
205 210 215
cag cag cac aca aat tac cat cag cag cct ctc ctt tagaaacaaa 1023
Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu
220 225
tcaagcattt tcttgaaagc cttcataagt gtattattca gtccttgtga taccaacctg 1083
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aaaatattaa aacttttttc cctctcaact caaaaggacc atgaataaat aaagcacaaa 1143
aacctctctt attctgaaaa aaaaaaaaaa at 1175

<210> 18
<211> 229
<212> PRT
<213> Homo sapiens

<400> 18
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20 25 30
Met Gly Pro Met Ile Asp Glu Lys Leu Glu Glu Ile Asp Arg Lys His
35 40 45
Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
50 55 60
Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
65 70 75 80
Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
85 90 95
Gln Thr Tyr Pro Val Gln Ser His Gly Asn Tyr Met Gly Gln Ser
100 105 110
Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
115 120 125
Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
130 135 140
Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
145 150 155 160
Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
165 170 175
Gly Thr Thr Ala Tyr Thr Gln Gln Met Gly Met Ser Val Asp Met Ser
180 185 190
Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro
195 200 205
Val Thr Val Pro Ala His Pro Val Ala Gln Gln His Thr Asn Tyr His
210 215 220
Gln Gln Pro Leu Leu
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<212> DNA
<213> Homo sapiens

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<220>
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<222> 112..813

<220>
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<222> 814..844

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                                         -15
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Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala
                                         -10
cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act 213
Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr
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gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg 261
Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val
                                         20
gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg 309
Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Thr Glu Glu Glu Val
                                         35
gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc aag gtg 357
Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val
                                         55
tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc 405
Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro
                                         70
acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat 453
Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn
                                         85
gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc 501
Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys
                                         100
acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc 549
Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile
                                         115
ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa 597
Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu
                                         135
ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg 645
Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu
                                         150
tat gag agg gat gag gac aac aac ctt ctg act gag aag cag aag ctg 693
Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu
                                         165
cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac 741
Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp
                                         180
cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg 789
His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg
                                         195
aag gcc aaa atc aag agt gag atg tagaaagttg taaaatagaa aaagtggagt 843
Lys Ala Lys Ile Lys Ser Glu Met
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t
                                         844

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<210> 20
 <211> 234
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

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  1      5      10      15
Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
      20      25      30
Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
      35      40      45
Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
      50      55      60
Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
      65      70      75
Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
  80      85      90      95
Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
      100      105      110
Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
      115      120      125
Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
      130      135      140
Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
      145      150      155
Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
  160      165      170      175
Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
      180      185      190
Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser
      195      200      205
Ala Arg Lys Ala Lys Ile Lys Ser Glu Met
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<210> 21
<211> 1997
<212> DNA
<213> Homo sapiens

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<220>
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<222> 1..126

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<221> CDS
<222> 127..1020

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<220>
<221> 3'UTR
<222> 1021..1997

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gctaaa atg aag act ctg cag tct aca ctt ctc ctg tta ctg ctt gtg 168
      Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Val
      -15                -10                -5
cct ctg ata aag cca gca cca cca acc cag cag gac tca cgc att atc 216
Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile
      1      5      10
tat gat tat gga aca gat aat ttt gaa gaa tcc ata ttt agc caa gat 264

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Tyr	Asp	Tyr	Gly	Thr	Asp	Asn	Phe	Glu	Glu	Ser	Ile	Phe	Ser	Gln	Asp		
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Tyr	Glu	Asp	Lys	Tyr	Leu	Asp	Gly	Lys	Asn	Ile	Lys	Glu	Lys	Glu	Thr		
	30					35					40						
gtg	ata	ata	ccc	aat	gag	aaa	agt	ctt	caa	tta	caa	aaa	gat	gag	gca	360	
Val	Ile	Ile	Pro	Asn	Glu	Lys	Ser	Leu	Gln	Leu	Gln	Lys	Asp	Glu	Ala		
	45				50				55					60			
ata	aca	cca	tta	cct	ccc	aag	aaa	gaa	aat	gat	gaa	atg	ccc	acg	tgt	408	
Ile	Thr	Pro	Leu	Pro	Pro	Lys	Lys	Glu	Asn	Asp	Glu	Met	Pro	Thr	Cys		
				65				70			75						
ctg	ctg	tgt	gtt	tgt	tta	agt	ggc	tct	gta	tac	tgt	gaa	gaa	gtt	gac	456	
Leu	Leu	Cys	Val	Cys	Leu	Ser	Gly	Ser	Val	Tyr	Cys	Glu	Glu	Val	Asp		
			80				85				90						
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Ile	Asp	Ala	Val	Pro	Pro	Leu	Pro	Lys	Glu	Ser	Ala	Tyr	Leu	Tyr	Ala		
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Arg	Phe	Asn	Lys	Ile	Lys	Lys	Leu	Thr	Ala	Lys	Asp	Phe	Ala	Asp	Ile		
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Pro	Asn	Leu	Arg	Arg	Leu	Asp	Phe	Thr	Gly	Asn	Leu	Ile	Glu	Asp	Ile		
	125				130					135					140		
gaa	gat	ggc	act	ttt	tca	aaa	ctt	tct	ctg	tta	gaa	gaa	ctt	tca	ctt	648	
Glu	Asp	Gly	Thr	Phe	Ser	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Leu	Ser	Leu		
				145				150			155						
gct	gaa	aat	caa	cta	cta	aaa	ctt	cca	ggt	ctt	cct	ccc	aag	ctc	act	696	
Ala	Glu	Asn	Gln	Leu	Leu	Lys	Leu	Pro	Val	Leu	Pro	Pro	Lys	Leu	Thr		
			160				165				170						
tta	ttt	aat	gca	aaa	tac	aac	aaa	atc	aag	agt	agg	gga	atc	aaa	gca	744	
Leu	Phe	Asn	Ala	Lys	Tyr	Asn	Lys	Ile	Lys	Ser	Arg	Gly	Ile	Lys	Ala		
	175					180					185						
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Asn	Ala	Phe	Lys	Lys	Leu	Asn	Asn	Leu	Thr	Phe	Leu	Tyr	Leu	Asp	His		
	190					195					200						
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Asn	Ala	Leu	Glu	Ser	Val	Pro	Leu	Asn	Leu	Pro	Glu	Ser	Leu	Arg	Val		
	205				210					215				220			
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Ile	His	Leu	Gln	Phe	Asn	Asn	Ile	Ala	Ser	Ile	Thr	Asp	Asp	Thr	Phe		
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tgc	aag	gct	aat	gac	acc	agt	tac	atc	cgg	gac	cgc	att	gaa	gag	ata	936	
Cys	Lys	Ala	Asn	Asp	Thr	Ser	Tyr	Ile	Arg	Asp	Arg	Ile	Glu	Glu	Ile		
			240					245			250						
cgc	ctg	gag	ggc	aat	cca	atc	gtc	ctg	gga	aag	cat	cca	aac	agt	ttt	984	
Arg	Leu	Glu	Gly	Asn	Pro	Ile	Val	Leu	Gly	Lys	His	Pro	Asn	Ser	Phe		
	255					260					265						
att	tgc	tta	aaa	aga	tta	ccg	ata	ggg	tca	tac	ttt	taacctctat				1030	
Ile	Cys	Leu	Lys	Arg	Leu	Pro	Ile	Gly	Ser	Tyr	Phe						
	270					275					280						
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ttcgaacaa	agtaatatga	aaatatatta	acagcattac	aaaatcctag	tttatactag	1270											
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<211> 1746
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 <213> Homo sapiens

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 <222> 10..1212

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<220>
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<220>
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 tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg 99
 Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val
 1 5 10
 ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta 147
 Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val
 15 20 25 30
 agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc 195
 Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
 35 40 45
 atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc 243
 Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly
 50 55 60
 atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg 291
 Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro
 65 70 75
 gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc 339
 Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
 80 85 90
 ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa 387
 Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
 95 100 105 110
 gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac 435
 Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
 115 120 125
 tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg 483
 Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
 130 135 140
 tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg 531
 Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
 145 150 155
 aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt 579

Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser		
160						165					170						
ggc	acc	acc	aac	ctt	cgt	ttg	ccc	aag	aaa	gtg	ttt	gaa	gct	gca	gtc	627	
Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val		
175					180					185					190		
aaa	tcc	atc	aag	gca	gcc	tcc	tcc	acg	gag	aag	ttc	cct	gac	ggc	ttc	675	
Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe		
				195					200					205			
tgg	cta	gga	gag	cag	ctg	gtg	tgc	tgg	caa	gca	ggc	acc	acc	cct	tgg	723	
Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp		
			210					215					220				
aac	att	ttc	cca	gtc	atc	tca	ctc	tac	cta	atg	ggc	gag	ggt	acc	aac	771	
Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn		
		225					230					235					
cag	tcc	ttc	cgc	atc	acc	atc	ctt	ccg	cag	caa	tac	ctg	cgg	cca	gtg	819	
Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val		
	240					245					250						
gaa	gat	gtg	gcc	acg	tcc	caa	gac	gac	tgt	tac	aag	ttt	gcc	atc	tca	867	
Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser		
255					260				265					270			
cag	tca	tcc	acg	ggc	act	ggt	atg	gga	gct	ggt	atc	atg	gag	ggc	ttc	915	
Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe		
			275					280					285				
tac	ggt	gtc	ttt	gat	cgg	gcc	cga	aaa	cga	att	ggc	ttt	gct	gtc	agc	963	
Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser		
			290					295					300				
gct	tgc	cat	gtg	cac	gat	gag	ttc	agg	acg	gca	gcg	gtg	gaa	ggc	cct	1011	
Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro		
		305				310						315					
ttt	gtc	acc	ttg	gac	atg	gaa	gac	tgt	ggc	tac	aac	att	cca	cag	aca	1059	
Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr		
	320				325				330								
gat	gag	tca	acc	ctc	atg	acc	ata	gcc	tat	gtc	atg	gct	gcc	atc	tgc	1107	
Asp	Glu	Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys		
335					340				345					350			
gcc	ctc	ttc	atg	ctg	cca	ctc	tgc	ctc	atg	gtg	tgt	cag	tgg	cgc	tgc	1155	
Ala	Leu	Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys		
			355					360					365				
ctc	cgc	tgc	ctg	cgc	cag	cag	cat	gat	gac	ttt	gct	gat	gac	atc	tcc	1203	
Leu	Arg	Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala	Asp	Asp	Ile	Ser		
		370						375					380				
ctg	ctg	aag	tgaggaggcc	catgggcaga	agatagggat	ccccctggac										1252	
Leu	Leu	Lys															
		385															
cacacctccg	tggttcactt	tggtcacaag	taggagacac	agatggcacc	tgtggccaga	1312											
gcacctcagg	accctcccca	cccaccaa	gcctctgcct	tgatggagaa	ggaaaaggct	1372											
ggcaaggtgg	gttcaggga	ctgtacctgt	aggagacaga	aaagagaaga	aagaagcact	1432											
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acttcagccc	tgaacctttg	tcaccattcc	tttaaattct	ccaacccaaa	gtattcttct	1552											
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taccctggca	gagaagagac	caagcttggt	tccctgctgg	ccaaagtcag	taggagagga	1672											
tgacagttt	gctatttgct	ttagagacag	ggactgtata	aacaagccta	acattggtgc	1732											
aaaaaaaaaa	aaaa					1746											

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 <213> Homo sapiens

<220>
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 <222> 1..17

<400> 24

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1				5					10					15	
Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile
			20						25					30	
Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr
		35						40					45		
Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu
	50						55					60			
Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Pro	Glu	Pro
65					70						75				
Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser
80				85						90				95	
Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu
			100						105					110	
Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu
			115						120				125		
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr
	130						135						140		
Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met
	145					150					155				
Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr
160					165					170				175	
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser
			180						185					190	
Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu
			195						200				205		
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile
	210						215					220			
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser
	225					230					235				
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp
240					245					250				255	
Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser
			260						265					270	
Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val
		275						280					285		
Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys
	290						295					300			
His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val
	305					310					315				
Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu
320					325					330				335	
Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala	Leu
			340						345					350	
Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu	Arg
		355					360						365		
Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala	Asp	Asp	Ile	Ser	Leu	Leu
	370						375					380			

Lys

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 <211> 1239

<212> DNA
<213> Homo sapiens

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<222> 1..126

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<222> 127..879

<220>
<221> 3'UTR
<222> 880..1239

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<221> polyA_site
<222> 1224..1239

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gccaggagag tcccgacagg agtgtcaggt ttcaatctca gcaccagcca ctgagagcag 120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc 168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
            -20              -15              -10
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca 216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
            -5              1              5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca 264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
            10              15              20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat 312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
            25              30              35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag 360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
            40              45              50              55
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc 408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
            60              65              70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg 456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
            75              80              85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc 504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
            90              95              100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag 552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
            105              110              115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg 600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Tyr Ser Gln Phe Leu
            120              125              130              135
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca 648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
            140              145              150
cgg cgg cac acc cgg agc gcc gag gac gac tcg gag cgg gac ccc ctg 696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
            155              160              165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt 744

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Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
      170                      175                      180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac      792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
      185                      190                      195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga      840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
200                      205                      210                      215
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggtcgct      889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
      220                      225
ggaagggcac cctctttaac ccatccctca gcaaacgcag ctcttcccaa ggaccaggtc 949
ccttgacgtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct 1009
gggggtccctt ccacaggagg tcctgtgaga accaaccttt gagggccaag tcatgggggtt 1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa 1129
ctagaaattt ccccttcattg aaggtagaga gaaggggtct ctccaacat atttctcttc 1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa 1239

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<210> 26
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 26

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Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
      -5                      1                      5
Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
      10                      15                      20
Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
25                      30                      35                      40
Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
      45                      50                      55
Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
      60                      65                      70
Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
      75                      80                      85
Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
      90                      95                      100
Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
105                      110                      115                      120
Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
      125                      130                      135
Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
      140                      145                      150
His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
      155                      160                      165
Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
      170                      175                      180
Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
185                      190                      195                      200
Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
      205                      210                      215
Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile

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220

225

<210> 27
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<220>
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<220>
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 <222> 116..961

<220>
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 <222> 962..1179

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 <222> 1145..1150

<220>
 <221> polyA_site
 <222> 1164..1179

<400> 27

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tggtctctctg actcacttct gacttttaggc gtcgaggac tgtgcccagg agcag atg 118
                                     Met
                                     1
cgg ctc aga gcc cag gtg cgc ctg ctt gag acc cgg gtc aaa cag caa 166
Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln
      5              10              15
cag gtc aag atc aag cag ctt ttg cag gag aat gaa gtc cag ttc ctt 214
Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu
      20              25              30
gat aaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag 262
Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln
      35              40              45
tat gca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga 310
Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly
50              55              60              65
ttt tac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat 358
Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr
      70              75              80
tgt gac atg tcc gat gga gga gga tgg act gta att cag aga cga tct 406
Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg Ser
      85              90              95
gat ggc agt gaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc 454
Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly
      100              105              110
ttt gga amt ttt gtc caa aaa cat ggt gaa tat tgg ctg ggc aat aaa 502
Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys
      115              120              125
aat ctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac 550
Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp
130              135              140              145

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ctt gca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc 598
Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe
150 155 160
aaa gtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat 646
Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr
165 170 175
tct gga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg 694
Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val
180 185 190
cag tgg tgg gct agt cac caa aga atg aaa ttc agc acg tgg gac aga 742
Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg
195 200 205
gat cat gac aac tat gaa ggg aac tgc gca gaa gaa gat cag tct ggc 790
Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly
210 215 220 225
tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac 838
Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr
230 235 240
agc ggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc 886
Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr
245 250 255
tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg 934
Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg
260 265 270
cca aat gat ttt att cca aat gta att taattgctgc tgttgggctt 981
Pro Asn Asp Phe Ile Pro Asn Val Ile
275 280
tcgtttctgc aattcagctt tgtttaaagt gatttgaaaa atactcattc tgaacatata 1041
catgcgcaat catgataact gttgtgagta gtgcttttca ttcttctcac ttgcctttgt 1101
tacttaatgt gctttcagta cagcagatat gcaatattca ccaaataaat gtagactgtg 1161
tcaaaaaaaaa aaaaaaaaa 1179

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<210> 28
 <211> 282
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 116
 <223> Xaa = Asn,Thr

<220>
 <221> UNSURE
 <222> 233
 <223> Xaa = Phe,Ser

<400> 28
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 Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe
 20 25 30
 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
 35 40 45
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
 50 55 60
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
 65 70 75 80
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg

	20		25		30		
gag	act	gtg	aaa	gga	gct	aaa	act
Glu	Thr	Val	Lys	Gly	Ala	Lys	Thr
	35		40		45		
aaa	ctt	cag	ggt	gat	tca	gag	gtc
Lys	Leu	Gln	Gly	Asp	Ser	Glu	Val
	50		55		60		65
gag	gat	tgt	ccg	ggt	gta	aaa	gag
Glu	Asp	Cys	Pro	Gly	Val	Lys	Glu
	70		75		80		
gga	ggt	ggc	cta	gag	gcc	aag	gcc
Gly	Gly	Gly	Leu	Glu	Ala	Lys	Ala
	85		90		95		
gaa	cag	gca	agt	gca	aag	gca	ggc
Glu	Gln	Ala	Ser	Ala	Lys	Ala	Gly
	100		105		110		
tct	ggg	aac	agg	acc	ctt	gca	ccg
Ser	Gly	Asn	Arg	Thr	Leu	Ala	Pro
	115		120		125		
ggt	gga	ggc	tgc	cac	ccc	acc	agg
Gly	Gly	Gly	Cys	His	Pro	Thr	Arg
	130		135		140		
gca	agt	gga	aaa	tcc	aag	gga	aag
Ala	Ser	Gly	Lys	Ser	Lys	Gly	Lys
	150		155		160		
cca	gct	aca	aca	tgg	cct	gtc	cgg
Pro	Ala	Thr	Thr	Trp	Pro	Val	Arg
	165		170		175		
aaa	att	gat	gat	att	ctg	agt	gct
Lys	Ile	Asp	Asp	Ile	Leu	Ser	Ala
	180		185		190		
atc	ctg	gag	cga	aca	aat	gat	cct
Ile	Leu	Glu	Arg	Thr	Asn	Asp	Pro
	195		200		205		
act	ctg	ggt	aac	aat	gca	gca	tat
Thr	Leu	Gly	Asn	Asn	Ala	Ala	Tyr
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Glu	Leu	Gly	Gly	Val	Pro	Ile	Ile
	230		235				

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 <222> 1..20

<220>
 <221> UNSURE
 <222> 49
 <223> Xaa = Glu, *

<400> 30
 Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile
 -20 -15 -10 -5
 Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp

				-25					-20					-15				
tgc	ggc	cag	gcg	tgg	ggt	gcg	tcg	gtg	ggc	ggc	cgc	agc	tgc	gag	gag			97
Cys	Gly	Gln	Ala	Trp	Gly	Ala	Ser	Val	Gly	Gly	Arg	Ser	Cys	Glu	Glu			
			-10					-5					1					
ctc	act	gcg	gtc	cta	acc	ccg	ccg	cag	ctc	ctc	gga	cgc	agg	ttt	aac			145
Leu	Thr	Ala	Val	Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn			
	5					10					15							
ttc	ttt	att	caa	caa	aaa	tgc	gga	ttc	aga	aaa	gca	ccc	agg	aag	gtt			193
Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val			
20					25					30				35				
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggt	gaa	gca	tac	aag	aga			241
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg			
				40				45						50				
agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc			289
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro			
			55					60					65					
tat	cct	ata	agg	agt	ctc	ata	aaa	cct	tta	ttt	ttt	act	gtt	ggg	ttt			337
Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe			
	70					75						80						
aca	ggc	tgt	gca	ttt	gga	tca	gct	gct	att	tgg	caa	tat	gaa	tca	ctg			385
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu			
	85				90					95								
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggt	ata	aaa	gct	gat	tgg	ttg			433
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu			
100					105					110				115				
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac			481
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn			
				120				125						130				
aag	tgg	tgg	aat	aac	cta	agt	gat	ggc	cag	cgg	act	gtg	aca	ggt	att			529
Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile			
			135					140					145					
ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg			577
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu			
	150					155						160						
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc			625
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val			
	165				170					175								
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt			673
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe			
	180				185					190				195				
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata			721
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile			
				200					205					210				
gtg	aac	att	ctg	ggt	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca			769
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala			
			215					220					225					
ggt	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggt	aaa	gtt	gcc	aca	gga			817
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly			
		230				235						240						
aga	tat	gga	cca	tca	ctt	ggt	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg			865
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met			
	245					250				255								
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca			913
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala			
260					265					270				275				
cat	ctt	ggg	gga	gct	ctt	ttt	gga	ata	tgg	tat	gtt	act	tac	ggt	cat			961
His	Leu	Gly	Gly	Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His			
				280					285					290				
gaa	ctg	att	tgg	aag	aac	agg	gag	ccg	cta	gtg	aaa	atc	tgg	cat	gaa			1009

Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu
 295 300 305
 ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg 1058
 ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Gly Ser Lys
 310 315 320
 attggacagt agtgggtgcat ctgggtccttg ccgcctgaga gccccaggag acatcgggcta 1118
 gagtgaccat ggctatgctc ccgtctggaa gatgccagca tctggcctcc cacttttttc 1178
 agctgtgtcc cccagtcctg gtcttttttag aatgtgaatg atgataaagt tgtgaaataa 1238
 aggtttctat ctagtttgca aaaaaaaaaa aaaaa 1273

 <210> 32
 <211> 345
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> 1..26

 <400> 32
 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala
 -25 -20 -15
 Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Leu Thr Ala Val
 -10 -5 1 5
 Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
 10 15 20
 Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
 25 30 35
 Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
 40 45 50
 Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
 55 60 65 70
 Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
 75 80 85
 Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
 90 95 100
 Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
 105 110 115
 Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
 120 125 130
 Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
 135 140 145 150
 Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
 155 160 165
 Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
 170 175 180
 Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
 185 190 195
 Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
 200 205 210
 Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
 215 220 225 230
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 235 240 245
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 250 255 260
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 265 270 275
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp

280 285 290
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 295 300 305 310
 Gly Pro Lys Lys Gly Gly Gly Ser Lys
 315

<210> 33
 <211> 723
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..72

<220>
 <221> CDS
 <222> 73..672

<220>
 <221> 3'UTR
 <222> 673..723

<220>
 <221> polyA_signal
 <222> 689..694

<220>
 <221> polyA_site
 <222> 708..723

<400> 33
 acaagaaaag aacatgggtct agactgaagt accaactaaa tcattctcctt tcaaattatc 60
 accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
 1 5 10
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
 15 20 25
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
 30 35 40 45
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
 50 55 60
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
 65 70 75
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val
 80 85 90
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr
 95 100 105
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447
 Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
 110 115 120 125
 ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
 Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu

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      130      135      140
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
      145      150      155
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
      160      165      170
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
      175      180      185
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
      190      195      200
aagatgtgtt aaaataaaaa aaaaaaaaaa t 723

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<210> 34
<211> 200
<212> PRT
<213> Homo sapiens

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<400> 34
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
1      5      10      15
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
      20      25      30
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
      35      40      45
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
      50      55      60
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
65      70      75      80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
      85      90      95
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
      100      105      110
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
      115      120      125
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
      130      135      140
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
145      150      155      160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
      165      170      175
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
      180      185      190
Asp Cys Asp Cys Glu Gln Cys Cys
      195      200

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<210> 35
<211> 845
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..118

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<220>
<221> CDS

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<222> 119..655

<220>

<221> 3'UTR

<222> 656..845

<220>

<221> polyA_signal

<222> 809..814

<220>

<221> polyA_site

<222> 830..845

<400> 35

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acaaatagcc ccggatatct gtgttaccag ccttgctctcg gccacctcaa ggataatcac 60
taaattctgc caaaaggact gaggaacggg gcctggaaaaa gggcaagaat atcacggc 118
atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695
Gly Pro Tyr
atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggg 755
attatctctc tatcagataa gattttgtta atgtactatt ttactottca ataaataaaa 815
cagtttatta tcgcaaaaaa aaaaaaaaaa 845
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<210> 36

<211> 179

<212> PRT

<213> Homo sapiens

<400> 36

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Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1          5          10          15
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20          25          30
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35          40          45
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50          55          60
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65          70          75          80
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85          90          95
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100         105         110
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115         120         125
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130         135         140
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145         150         155         160
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165         170         175
Gly Pro Tyr
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<210> 37

<211> 517

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..16

<220>

<221> CDS

<222> 17..259

<220>

<221> 3'UTR

<222> 260..517

<400> 37

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ttccatagaa tgggag atg tca cca ggg cag cct atg aca ttc ccc cca gag 52
          Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu
          1          5          10
gcc ctg tgg gtg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100
Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu
15          20          25
gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148
Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu
30          35          40
gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196
Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser
45          50          55          60
aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244
Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp
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```

          65          70          75
gga caa gaa ata gcc tgaccatgag gaccagggag ctgctacccc tccctacagc 299
Gly Gln Glu Ile Ala
          80
tcctaccctc tggctgcaat ggggctgcac tgtgagccct gcccccaaca gatgcatcct 359
gctctgacag gtgggctcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419
tttctccaat ggacatgatt cccaagtcat cctgctgcct tttttcttat agacacaatg 479
aacagaccac ccacaacctt agttctctaa gtcacccct 517

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<210> 38
 <211> 81
 <212> PRT
 <213> Homo sapiens

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<400> 38
Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val
1          5          10          15
Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
          20          25          30
Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala
          35          40          45
Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
          50          55          60
Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
65          70          75          80
Ala

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<210> 39
 <211> 1816
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..259

<220>
 <221> CDS
 <222> 260..1048

<220>
 <221> 3'UTR
 <222> 1049..1816

<220>
 <221> polyA_signal
 <222> 1782..1787

<220>
 <221> polyA_site
 <222> 1801..1816

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<400> 39
actctggggc cattgccagc cggctgtagg cattcagggc agtgtcttct gcattctcta 60
ggaacctcgg gaggcgcagc tccggcgctt ggtagcgaga ggcggggtcc ggagatcccg 120
gcctcacttc gtcccactgt ggtaggggt gagtctctgc aatgttaagt gatttgctca 180
aggtgcccac ttcgcaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240
aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
          Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu

```


gaccgtcttg actggctgga gccttcaaag ccactgggat gtcctccagg cacctggggtc 1718
 ccatgaccag ctccccgtct ccataggggt aggcatttca ctggtttatg aagctcgagt 1778
 ttcattaaat atgttaagaa tcaaaaaaaaa aaaaaaaaa 1816

<210> 40
 <211> 263
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<400> 40
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu Leu Leu Gly Ser Leu
 -20 -15 -10 -5
 Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp Met Gln Tyr Trp Arg
 1 5 10
 Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro
 15 20 25
 Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu
 30 35 40
 Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys
 45 50 55 60
 Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val
 65 70 75
 Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn
 80 85 90
 Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe
 95 100 105
 Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
 110 115 120
 Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly
 125 130 135 140
 Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn
 145 150 155
 Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser
 160 165 170
 Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val
 175 180 185
 Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys
 190 195 200
 Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Leu Gln Leu
 205 210 215 220
 Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly
 225 230 235
 Arg Gln Pro Tyr Lys Ser Trp
 240

<210> 41
 <211> 643
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..90

<220>

<221> CDS
<222> 91..462

<220>
<221> 3'UTR
<222> 463..643

<220>
<221> polyA_signal
<222> 607..612

<220>
<221> polyA_site
<222> 628..643

<400> 41
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cacacctgca cccgcgccg gcatagcacc atg cct gct tgt cgc cta ggc ccg 114
Met Pro Ala Cys Arg Leu Gly Pro
-25
cta gcc gcc gcc ctc ctc ctc agc ctg ctg ctg ttc ggc ttc acc cta 162
Leu Ala Ala Ala Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu
-20 -15 -10
gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210
Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln
-5 1 5 10
gct gac cag aac tgc acg caa gag tgc gtc tgc gac agc gaa tgc gcc 258
Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
15 20 25
gac aac ctc aag tgc tgc agc ggc ggc tgt gcc acc ttc tgc tct ctg 306
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
30 35 40
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
45 50 55
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
60 65 70 75
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
80 85 90
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
Thr Pro Asn Phe
95
agttttctgcc tggccctgca tctgggtcca gcccaactgc cctccccttt ttccgggactc 562
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
tcagcaaaaa aaaaaaaaaa a 643

<210> 42
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..30

<400> 42
Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser

-30					-25				-20				-15		
Leu	Leu	Leu	Phe	Gly	Phe	Thr	Leu	Val	Ser	Gly	Thr	Gly	Ala	Glu	Lys
				-10					-5					1	
Thr	Gly	Val	Cys	Pro	Glu	Leu	Gln	Ala	Asp	Gln	Asn	Cys	Thr	Gln	Glu
		5					10					15			
Cys	Val	Ser	Asp	Ser	Glu	Cys	Ala	Asp	Asn	Leu	Lys	Cys	Cys	Ser	Ala
	20					25					30				
Gly	Cys	Ala	Thr	Phe	Cys	Ser	Leu	Pro	Asn	Asp	Lys	Glu	Gly	Ser	Cys
35					40					45					50
Pro	Gln	Val	Asn	Ile	Asn	Phe	Pro	Gln	Leu	Gly	Leu	Cys	Arg	Asp	Gln
				55					60					65	
Cys	Gln	Val	Asp	Ser	Gln	Cys	Pro	Gly	Gln	Met	Lys	Cys	Cys	Arg	Asn
			70					75					80		
Gly	Cys	Gly	Lys	Val	Ser	Cys	Val	Thr	Pro	Asn	Phe				
		85					90								

<210> 43
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..227

<220>
 <221> CDS
 <222> 228..501

<400> 43
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 agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
 ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
 ccatggtgcc caaggaaagc ccttgaagct caccaggagg aagaagc atg cag ggc 236
 Met Gln Gly
 -30
 act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
 Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
 -25 -20 -15
 aca ctg ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
 Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
 -10 -5 1
 aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
 Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
 5 10 15
 cag ctt tca ctt ctg ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
 Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
 20 25 30 35
 gac ttc tgg cgt ggc cca gcc agg ccc agc ctg cct gtg gat atg aga 476
 Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
 40 45 50
 gtt cct ttc tcc gaa ctg aaa gac a 501
 Val Pro Phe Ser Glu Leu Lys Asp
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<210> 44
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..33

<400> 44
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 Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
 -15 -10 -5
 Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
 1 5 10 15
 Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
 20 25 30
 Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
 35 40 45
 Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
 50 55

<210> 45
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 <212> DNA
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<220>
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 <222> 1..97

<220>
 <221> CDS
 <222> 98..934

<220>
 <221> 3'UTR
 <222> 935..960

<400> 45
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 cggcccgttt caccgagagg aggaaggaca ctgggtc atg acg cca tca gaa ggc 115
 Met Thr Pro Ser Glu Gly
 1 5
 gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163
 Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu
 10 15 20
 gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg 211
 Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly
 25 30 35
 cgc agt ctc ttg aag gcg ctt gtc aag aaa tct gca ctg tgt ggg gag 259
 Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu
 40 45 50
 caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307
 Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu
 55 60 65 70
 ggt ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355
 Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe
 75 80 85
 aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403
 Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly
 90 95 100

ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct	451
Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro	
105 110 115	
gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc	499
Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Arg Leu Pro	
120 125 130	
tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct	547
Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser	
135 140 145 150	
tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg	595
Cys Pro Gly Asp Ser Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu	
155 160 165	
cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc	643
Leu His Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser	
170 175 180	
ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg	691
Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser	
185 190 195	
gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act	739
Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr	
200 205 210	
cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg	787
Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly	
215 220 225 230	
ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccg gta	835
Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Pro Val	
235 240 245	
tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt	883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly	
250 255 260	
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga	931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly	
265 270 275	
ttc tagggatggg gcagagtggc agcatc	960
Phe	

<210> 46

<211> 279

<212> PRT

<213> Homo sapiens

<400> 46

Met Thr Pro Ser Glu Gly Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu	
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20 25 30	
Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys	
35 40 45	
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser	
50 55 60	
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu	
65 70 75 80	
Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu	
85 90 95	
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys	
100 105 110	
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp	
115 120 125	
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala	

130 135 140
 Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys
 145 150 155 160
 Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
 165 170 175
 Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
 180 185 190
 Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
 195 200 205
 Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
 210 215 220
 Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
 225 230 235 240
 Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
 245 250 255
 Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
 260 265 270
 Trp Gly Trp Gly Gln Gly Phe
 275

<210> 47
 <211> 1294
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..266

<220>
 <221> CDS
 <222> 267..1139

<220>
 <221> 3'UTR
 <222> 1140..1294

<220>
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 <222> 1246..1251

<220>
 <221> polyA_site
 <222> 1279..1294

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 aaattcttac ctgctcttt cactgctagt aagatcagat tgcgtttctt tcagttactc 120
 ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
 ttcaatacct ggaaggaaaa aaaaaataac ctcaactccg ttttgaaaaa aacattccaa 240
 gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
 Met Ile Tyr Thr Met Lys Lys Val His
 -25 -20
 gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
 Ala Leu Trp Ala Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro
 -15 -10 -5
 ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
 1 5 10

acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag	437
Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys	
15 20 25 30	
gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat	485
Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn	
35 40 45	
att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga	533
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly	
50 55 60	
aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca	581
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr	
65 70 75	
aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt	629
Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys	
80 85 90	
cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt	677
Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys	
95 100 105 110	
gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag	725
Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu	
115 120 125	
aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc	773
Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe	
130 135 140	
cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg	821
Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu	
145 150 155	
act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc	869
Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro	
160 165 170	
tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag	917
Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu	
175 180 185 190	
aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag	965
Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys	
195 200 205	
tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa	1013
Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu	
210 215 220	
tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga	1061
Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly	
225 230 235	
ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata	1109
Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile	
240 245 250	
gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt	1159
Ala Tyr Glu Glu Ile Phe Val Lys Asn Met	
255 260	
aacattaatt ctactaaata ttttatatga aatgtttcac tatgattttc tatttttctt	1219
ctaaaatgct tttaattaat atgttcatta aattttctat gcttattgta cttgttacca	1279
aaaaaaaaaaaa	1294

<210> 48
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> 1..28

<400> 48

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-10 -5 1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5 10 15 20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
25 30 35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
40 45 50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
55 60 65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
70 75 80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
85 90 95 100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
105 110 115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
120 125 130
Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
135 140 145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
150 155 160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165 170 175 180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
185 190 195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
200 205 210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
215 220 225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
230 235 240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245 250 255 260
Lys Asn Met

<210> 49

<211> 1194

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..47

<220>

<221> CDS

<222> 48..1100

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<221> 3'UTR

<222> 1101..1194

<220>

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<222> 1159..1164

<220>
<221> polyA_site
<222> 1179..1194

<400> 49

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                                     Met Pro Ser
tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc      104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20                                     -15      -10      -5
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag      152
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
                                     1      5      10
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa      200
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
                                     15      20      25
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc      248
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
                                     30      35      40
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta      296
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
                                     45      50      55      60
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc      344
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
                                     65      70      75
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac      392
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
                                     80      85      90
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag      440
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
                                     95      100      105
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt      488
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
                                     110      115      120
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag      536
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
                                     125      130      135      140
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag      584
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
                                     145      150      155
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg      632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
                                     160      165      170
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg      680
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
                                     175      180      185
cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat      728
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp
                                     190      195      200
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta      776
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu
                                     205      210      215      220
cat tta ccc aaa ctg tcc att act gga acc tat gat ctg aag agc gtc      824
His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val
                                     225      230      235
ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg gct gac ctc      872

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Leu Gly Gln	Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu	
240	245	250
tcc ggg gtc	aca gag gag gca ccc ctg aag ctc tcc aag gcc gtg cat	920
Ser Gly Val Thr	Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His	
255	260	265
aag gct gtg	ctg acc atc gac gag aaa ggg act gaa gct gct ggg gcc	968
Lys Ala Val	Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala	
270	275	280
atg ttt tta	gag gcc ata ccc atg tct atc ccc ccc gag gtc aag ttc	1016
Met Phe Leu	Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe	
285	290	295
aac aaa ccc	ttt gtc ttc tta atg att gac caa aat acc aag tct ccc	1064
Asn Lys Pro	Phe Val Phe Leu Met Ile Asp Gln Asn Thr Lys Ser Pro	
305	310	315
ctc ttc atg	gga aaa gtg gtg aat ccc acc caa aaa taactgcctc	1110
Leu Phe Met	Gly Lys Val Val Asn Pro Thr Gln Lys	
320	325	
tcgctcctca	acccctcccc tccatccctg gccccctccc tggatgacat taaagaagg	1170
ttgagctgaa	aaaaaaaaaaaa aaaa	1194

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 <211> 351
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..24

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Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln	5
10	15
Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp	20
25	30
Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly	35
45	50
Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His	55
60	65
Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys	70
75	80
Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp	85
90	95
Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr	100
105	110
Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr	115
125	130
Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro	135
140	145
Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu	150
155	160
Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile	165
170	175
Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu	180
185	190
Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser	195
	200

Ser	Phe	Cys	Ala	Phe	Lys	Ser	Asp	Asp	Gly	Pro	Cys	Lys	Ala	Ile	Met	
25					30				35						40	
aaa	aga	ttt	ttc	ttc	aat	att	ttc	act	cga	cag	tgc	gaa	gaa	ttt	ata	538
Lys	Arg	Phe	Phe	Phe	Asn	Ile	Phe	Thr	Arg	Gln	Cys	Glu	Glu	Phe	Ile	
				45					50					55		
tat	ggg	gga	tgt	gaa	gga	aat	cag	aat	cga	ttt	gaa	agt	ctg	gaa	gag	586
Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser	Leu	Glu	Glu	
			60					65					70			
tgc	aaa	aaa	atg	tgt	aca	aga	gaa	aag	cca	gat	ttc	tgc	ttt	ttg	gaa	634
Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys	Phe	Leu	Glu	
			75				80					85				
gaa	gat	cct	gga	ata	tgt	cga	ggg	tat	att	acc	agg	tat	ttt	tat	aac	682
Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr	Phe	Tyr	Asn	
			90			95					100					
aat	cag	aca	aaa	cag	tgt	gaa	cgt	ttc	aag	tat	ggg	gga	tgc	ctg	ggc	730
Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly	Cys	Leu	Gly	
				110						115				120		
aat	atg	aac	aat	ttt	gag	aca	ctg	gaa	gaa	tgc	aag	aac	att	tgt	gaa	778
Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu	
				125						130				135		
gat	ggg	ccg	aat	ggg	ttc	cag	gtg	gat	aat	tat	gga	acc	cag	ctc	aat	826
Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn	
			140					145					150			
gct	gtg	aat	aac	tcc	ctg	act	ccg	caa	tca	acc	aag	gtt	ccc	agc	ctt	874
Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu	
			155				160					165				
ttt	gaa	ttt	cac	ggg	ccc	tca	tgg	tgt	ctc	act	cca	gca	gac	aga	gga	922
Phe	Glu	Phe	His	Gly	Pro	Ser	Trp	Cys	Leu	Thr	Pro	Ala	Asp	Arg	Gly	
			170			175					180					
ttg	tgt	cgt	gcc	aat	gag	aac	aga	ttc	tac	tac	aat	tca	gtc	att	ggg	970
Leu	Cys	Arg	Ala	Asn	Glu	Asn	Arg	Phe	Tyr	Tyr	Asn	Ser	Val	Ile	Gly	
					190					195				200		
aaa	tgc	cgc	cca	ttt	aag	tac	agt	gga	tgt	ggg	gga	aat	gaa	aac	aat	1018
Lys	Cys	Arg	Pro	Phe	Lys	Tyr	Ser	Gly	Cys	Gly	Gly	Asn	Glu	Asn	Asn	
				205					210					215		
ttt	act	tcc	aaa	caa	gaa	tgt	ctg	agg	gca	tgt	aaa	aaa	ggg	ttc	atc	1066
Phe	Thr	Ser	Lys	Gln	Glu	Cys	Leu	Arg	Ala	Cys	Lys	Lys	Gly	Phe	Ile	
			220					225					230			
caa	aga	ata	tca	aaa	gga	ggc	cta	att	aaa	acc	aaa	aga	aaa	aga	aag	1114
Gln	Arg	Ile	Ser	Lys	Gly	Gly	Leu	Ile	Lys	Thr	Lys	Arg	Lys	Arg	Lys	
			235				240				245					
aag	cag	aga	gtg	aaa	ata	gca	tat	gaa	gaa	att	ttt	gtt	aaa	aat	atg	1162
Lys	Gln	Arg	Val	Lys	Ile	Ala	Tyr	Glu	Glu	Ile	Phe	Val	Lys	Asn	Met	
			250			255					260					
tga	at	ttt	ggt	atag	caat	gtt	aac	at	taatt	ctact	aaata	ttttat	atga	aat	gttttcac	1222
tat	gatt	tttc	tatt	tttt	ttct	ctaaa	atgct	ttta	at	taatt	at	atgt	ttcatta	aatt	ttttctat	1282
gct	tatt	gtga	ctt	gttat	ca	aaaaaaaa	aaaaa									1317

<210> 52
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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..28

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<221> polyA_site
<222> 1892..1907

<400> 53

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gtatctctta	ggaagcaagc	ataggaaaca	ggcccatccg	tctgcctgtt	ttgcttcctc	180
atctcacttc	tacacgaggg	tgcctgtgct	caattgctgt	tttcccctaa	agagactctt	240
ttccataagt	ttgtgaaatg	ccatcgacaa	acctgatcgc	attgcatttc	actctgctgt	300
tgagtcgatt	tttctttatt	ttatcattta	gtaactcctt	gctctacaga	gctttcacct	360
tccacatatt	tcagattcat	tctttcctaa	actatgtggg	ggctctacgtc	ctcactgact	420
tatcaacatg	ctaccatcat	gcacttccta	tctctattcc	tcttctttaa	atttggttcc	480
aaatggctca	caccattatt	ctgagctatt	acctgcctac	gcagtcctag	aaagtaagtg	540
attcaggaaa	cattccccaa	aagtaaagtt	tctcaggtaa	gatcagaaga	ctcccatgag	600
tcactgctgc	tcaggatcac	atctggctcc	ttgaagagtg	attcatcaga	ccttacatag	660
atcttgtcat	aaaaatgaaa	gaggcctcgg	gggaaggctt	tgggctgggtg	gcttctgttg	720
gagtcctggg	ctgtgggggtg	aaagccgtgg	ctgtagagct	tcatgcggag	ttacttagct	780
ttgctctcct	gtggacaggc	catgcctgtg	cctcccccaa	gcacgcggaaa	aattggcata	840
gatggggcct	tctcaaaaat	cccactcctg	gagcactggc	caaaaattact	accatcctga	900
tgctgggctt	gcagtccttt	cctttgggaa	tatgaacatg	gtcaaaaatta	agtgaacgtg	960
tctttctggc	tttctgtaca	atggagcaga	acaaagtatc	aatttaacta	aaatttgaac	1020
taaatcctct	ttccaggttt	gga atg cac	ttc tgt gga	ggc acc ttg	ata tcc	1073
		Met His Phe Cys Gly Gly Thr Leu Ile Ser				
		1	5	10		
cca gag tgg	gtg ttg act	gct gcc cac	tgc ttg gag	aag tcc cca	agg	1121
Pro Glu Trp	Val Leu Thr	Ala Ala His	Cys Leu Glu	Lys Ser Pro	Arg	
	15	20	25			
cct tca tcc	tac aag gtc	atc ctg ggt	gca cac caa	gaa gtg aat	ctc	1169
Pro Ser Ser	Tyr Lys Val	Ile Leu Gly	Ala His Gln	Glu Val Asn	Leu	
	30	35	40			
gaa ccg cat	gtt cag gaa	ata gaa gtg	tct agg ctg	ttc ttg gag	ccc	1217
Glu Pro His	Val Gln Glu	Ile Glu Val	Ser Arg Leu	Phe Leu Glu	Pro	
	45	50	55			
aca cga aaa	gat att gcc	ttg cta aag	cta agc agt	cct gcc gtc	atc	1265
Thr Arg Lys	Asp Ile Ala	Leu Leu Lys	Leu Ser Ser	Pro Ala Val	Ile	
	60	65	70			
act gac aaa	gta atc cca	gct tgt ctg	cca tcc cca	aat tat gtg	gtc	1313
Thr Asp Lys	Val Ile Pro	Ala Cys Leu	Pro Ser Pro	Asn Tyr Val	Val	
	75	80	85	90		
gct gac cgg	acc gaa tgt	ttc atc act	ggc tgg gga	gaa acc caa	ggg	1361
Ala Asp Arg	Thr Glu Cys	Phe Ile Thr	Gly Trp Gly	Glu Thr Gln	Gly	
	95	100	105			
act ttt gga	gct ggc ctt	ctc aag gaa	gcc cag ctc	cct gtg att	gag	1409
Thr Phe Gly	Ala Gly Leu	Leu Lys Glu	Ala Gln Leu	Pro Val Ile	Glu	
	110	115	120			
aat aaa gtg	tgc aat cgc	tat gag ttt	ctg aat gga	aga gtc caa	tcc	1457
Asn Lys Val	Cys Asn Arg	Tyr Glu Phe	Leu Asn Gly	Arg Val Gln	Ser	
	125	130	135			
acc gaa ctc	tgt gct ggg	cat ttg gcc	gga ggc act	gac agt tgc	cag	1505
Thr Glu Leu	Cys Ala Gly	His Leu Ala	Gly Gly Thr	Asp Ser Cys	Gln	
	140	145	150			
ggg gac agt	gga ggt cct	ctg gtt tgc	ttc gag aag	gac aaa tac	att	1553
Gly Asp Ser	Gly Gly Pro	Leu Val Cys	Phe Glu Lys	Asp Lys Tyr	Ile	
	155	160	165	170		
tta caa gga	gtc act tct	tgg ggt ctt	ggc tgt gca	cgc ccc aat	aag	1601
Leu Gln Gly	Val Thr Ser	Trp Gly Leu	Gly Cys Ala	Arg Pro Asn	Lys	
	175	180	185			
cct ggt gtc	tat gtt cgt	gtt tca agg	ttt gtt act	tgg att gag	gga	1649
Pro Gly Val	Tyr Val Arg	Val Ser Arg	Phe Val Thr	Trp Ile Glu	Gly	

190 195 200
 gtg atg aga aat aat taattggacg ggagacagag tgacgcactg actcacctag 1704
 Val Met Arg Asn Asn

205
 aggctggaac gtgggtaggg atttagcatg ctggaaataa ctggcagtaa tcaaacgaag 1764
 aactgtccc cagctaccag ctatgccaaa cctcggcatt ttttgtgtta ttttctgact 1824
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 aactttgaaa aaaaaaaaaa aaa 1907

<210> 54
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 54
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 20 25 30
 Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
 35 40 45
 Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
 50 55 60
 Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
 65 70 75 80
 Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
 85 90 95
 Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
 100 105 110
 Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg
 115 120 125
 Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
 130 135 140
 His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 145 150 155 160
 Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
 165 170 175
 Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
 180 185 190
 Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
 195 200 205

<210> 55
 <211> 809
 <212> DNA
 <213> Homo sapiens

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 <222> 26..628

<220>
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 <222> 629..809

<220>

<221> polyA_signal

<222> 766..771

<220>

<221> polyA_site

<222> 795..809

<400> 55

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                               1                               5
gga cct gga aga gta cca ggg gcc aca gca ggg atg aat gga gtg gac 100
Gly Pro Gly Arg Val Pro Gly Ala Thr Ala Gly Met Asn Gly Val Asp
10                               15                               20                               25
acg tcg ctt ctc tgt gat ttg ttg cag gcc ctg acc ttc ctg acc aga 148
Thr Ser Leu Leu Cys Asp Leu Leu Gln Ala Leu Thr Phe Leu Thr Arg
                               30                               35                               40
aat gaa att ctg tgc atc cat gac acc ttc ctg aag ctc tgc cct cct 196
Asn Glu Ile Leu Cys Ile His Asp Thr Phe Leu Lys Leu Cys Pro Pro
                               45                               50                               55
ggg aag tac tac aag gag gca acg ctc acc atg gac cag gtc agc tcc 244
Gly Lys Tyr Tyr Lys Glu Ala Thr Leu Thr Met Asp Gln Val Ser Ser
                               60                               65                               70
ctg cca gct ctg cgg gtc aac cct ttc aga gac cgt atc tgc aga gtg 292
Leu Pro Ala Leu Arg Val Asn Pro Phe Arg Asp Arg Ile Cys Arg Val
                               75                               80                               85
ttc tcc cac aaa ggc atg ttc tcc ttt gag gat gtg ctg ggc atg gca 340
Phe Ser His Lys Gly Met Phe Ser Phe Glu Asp Val Leu Gly Met Ala
90                               95                               100                               105
tct gtg ttc agc gag cag gcc tgc cca agc ctg aag att gag tat gcc 388
Ser Val Phe Ser Glu Gln Ala Cys Pro Ser Leu Lys Ile Glu Tyr Ala
                               110                               115                               120
ttt cgc atc tat gat ttt aat gag aat ggc ttc att gat gag gag gat 436
Phe Arg Ile Tyr Asp Phe Asn Glu Asn Gly Phe Ile Asp Glu Glu Asp
                               125                               130                               135
ctg cag agg atc atc ctg cga ctg ctg aac agt gat gac atg tct gag 484
Leu Gln Arg Ile Ile Leu Arg Leu Leu Asn Ser Asp Asp Met Ser Glu
                               140                               145                               150
gac ctc ctg atg gac ctc acg aac cac gtc ctg agt gag tcg gat ctg 532
Asp Leu Leu Met Asp Leu Thr Asn His Val Leu Ser Glu Ser Asp Leu
                               155                               160                               165
gac aat gac aac atg ctg tcc ttc tca gag ttt gaa cat gca atg gcc 580
Asp Asn Asp Asn Met Leu Ser Phe Ser Glu Phe Glu His Ala Met Ala
170                               175                               180                               185
aag tct cca gat ttc atg aac tcc ttt cgg att cac ttc tgg gga tgc 628
Lys Ser Pro Asp Phe Met Asn Ser Phe Arg Ile His Phe Trp Gly Cys
                               190                               195                               200
tgatgtagcg gcaaatacct gacatggcag cctcgaggga gaccacagga atcgaacccc 688
ctccagcact ggaggagct gggttgaagt atgactttgt actgggcca cactcacctc 748
tagaatattg tttattagat aaaagaaaaa gcttttcctt agcccgaaaa aaaaaaaaaa 808
t                                                                    809
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<210> 56

<211> 201

<212> PRT

<213> Homo sapiens

<400> 56

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Ala	Thr	Ala	Gly	Met	Asn	Gly	Val	Asp	Thr	Ser	Leu	Leu	Cys	Asp	Leu
		20						25					30		
Leu	Gln	Ala	Leu	Thr	Phe	Leu	Thr	Arg	Asn	Glu	Ile	Leu	Cys	Ile	His
	35					40						45			
Asp	Thr	Phe	Leu	Lys	Leu	Cys	Pro	Pro	Gly	Lys	Tyr	Tyr	Lys	Glu	Ala
50					55						60				
Thr	Leu	Thr	Met	Asp	Gln	Val	Ser	Ser	Leu	Pro	Ala	Leu	Arg	Val	Asn
65				70						75				80	
Pro	Phe	Arg	Asp	Arg	Ile	Cys	Arg	Val	Phe	Ser	His	Lys	Gly	Met	Phe
			85					90						95	
Ser	Phe	Glu	Asp	Val	Leu	Gly	Met	Ala	Ser	Val	Phe	Ser	Glu	Gln	Ala
		100					105						110		
Cys	Pro	Ser	Leu	Lys	Ile	Glu	Tyr	Ala	Phe	Arg	Ile	Tyr	Asp	Phe	Asn
	115					120						125			
Glu	Asn	Gly	Phe	Ile	Asp	Glu	Glu	Asp	Leu	Gln	Arg	Ile	Ile	Leu	Arg
	130				135					140					
Leu	Leu	Asn	Ser	Asp	Asp	Met	Ser	Glu	Asp	Leu	Leu	Met	Asp	Leu	Thr
145				150					155					160	
Asn	His	Val	Leu	Ser	Glu	Ser	Asp	Leu	Asp	Asn	Asp	Asn	Met	Leu	Ser
			165					170						175	
Phe	Ser	Glu	Phe	Glu	His	Ala	Met	Ala	Lys	Ser	Pro	Asp	Phe	Met	Asn
		180					185						190		
Ser	Phe	Arg	Ile	His	Phe	Trp	Gly	Cys							
	195						200								

<210> 57

<211> 1133

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..475

<220>

<221> CDS

<222> 476..964

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<220>

<221> polyA_site

<222> 1118..1133

<400> 57

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ccccccagga	tctgaaggcc	tcccaggccc	cccaggccca	gcgggtccca	gaggagagcg		180
aggaccccaa	ggtaactccg	gtgagaagg	cgaccaggga	tttcaaggcc	agccaggctt		240
tccgggcccc	ccgggtcccc	ctggattccc	aggcaaagtt	ggatcacctg	gcccacctgg		300
ccctcaagca	gagaagggca	gcgaagggat	tcgaggccca	tcaggcctgc	ctggctcccc		360

tgggccaccg ggacctcctg ggattcaggg ccccgccggt ctggatgggt tggatgggaa 420
 ggatggcaag cctggcttga ggggggaccc tggctctgct ggccccctg gactc atg 478
 Met
 1
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
 5 10 15
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
 20 25 30
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
 35 40 45
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
 50 55 60 65
 cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
 Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
 70 75 80
 gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
 Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
 85 90 95
 cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
 Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
 100 105 110
 ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
 Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
 115 120 125
 cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
 Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
 130 135 140 145
 atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
 Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
 150 155 160
 ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
 Phe Gly
 ccaaagctta taggactctg tgacaggttg tgaatgtttt ttttgttggt gttgttggtt 1074
 ttaattgctg ttaatatattt ttaaataata aagaacacaa actaaaaaaaa aaaaaaaaaa 1133

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
 50 55 60
 Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
 65 70 75 80
 Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
 85 90 95
 Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
 100 105 110

Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
115 120 125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
130 135 140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
145 150 155 160
Pro Phe Gly

<210> 59
<211> 838
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..78

<220>
<221> CDS
<222> 79..642

<220>
<221> 3'UTR
<222> 643..838

<220>
<221> polyA_signal
<222> 799..804

<220>
<221> polyA_site
<222> 823..838

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cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
1 5 10
aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
15 20 25
aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg 207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
30 35 40
gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
45 50 55
gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
60 65 70 75
gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
80 85 90
gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
95 100 105
gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
110 115 120

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cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
125 130 135
gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
140 145 150 155
tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
160 165 170
gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
175 180 185
aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg caccacacct 692
Lys
gacccctccc tcagctgtcc tgtgccccgc cctctcccgc acactcagtc cccctgacctg 752
gcgttcctgc cgcagctctg acctggtgct gtcgccctgg catcttaata aamcctgctt 812
atacttcctt aaaaaaaaaa aaaaaa 838

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<210> 60
 <211> 188
 <212> PRT
 <213> Homo sapiens

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<400> 60
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20 25 30
Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
35 40 45
Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
50 55 60
Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
65 70 75 80
Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
85 90 95
Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe
100 105 110
Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala
115 120 125
Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu
130 135 140
Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met
145 150 155 160
Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu
165 170 175
Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
180 185

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<210> 61
 <211> 862
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..158

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<221> CDS
 <222> 159..764

<220>
 <221> 3'UTR
 <222> 765..862

<400> 61
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 tggctgctgc cttaagacgt gcagcctggg cctgtggctgt cactgcgttc ggacccagac 120
 ccgctgcagg cagcagcagc ccccgcccgc gcagcagc atg gag ctc tgg ggg gcc 176
 Met Glu Leu Trp Gly Ala
 -20 -15
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu
 -10 -5 1
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
 5 10 15
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
 Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
 20 25 30
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Ala Leu Gln Thr Val
 35 40 45 50
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
 55 60 65
 cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tgc cgc ggg 464
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
 70 75 80
 ggc acc ctg agc acc cct cag act ggc tgc gag aac gac gcc ctg tat 512
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
 85 90 95
 gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560
 Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
 100 105 110
 ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608
 Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
 115 120 125 130
 cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
 Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
 135 140 145
 ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
 Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
 150 155 160
 aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
 Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
 165 170 175
 ttc ggg atc gtg tagccggcgg ggcggggggc gtggggggggc tggaggaggg 804
 Phe Gly Ile Val
 180
 caggagccgc gggaggccgg gaggagggtg gggaccttgc agcccccatc ctctccgt 862

<210> 62
 <211> 202
 <212> PRT
 <213> Homo sapiens

<400> 62

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<210> 63
<211> 618
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 195..587
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<220>  
<221> polyA_signal  
<222> 578..583
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<400> 63
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ttcgtttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180
acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
                Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu
                -20                -15                -10
act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala
                -5                1                5
cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326
Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln
                10                15                20
agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala
                25                30                35
tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422
Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr
40                45                50                55
aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
                60                65                70
atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
                75                80                85
act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
                90                95                100
tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
Cys Phe Ala Leu Leu Asn Cys
                105                110

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<210> 64
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..22

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<400> 64
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Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
                -5                1                5                10
Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
                15                20                25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
                30                35                40
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Ser Leu Ala
                45                50                55
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
                60                65                70
Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg Thr Ala Gly Ala
                75                80                85                90
Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met Cys Phe Ala Leu
                95                100                105
Leu Asn Cys

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<210> 65

<211> 836
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..176

<220>
 <221> CDS
 <222> 177..767

<220>
 <221> 3'UTR
 <222> 768..836

<220>
 <221> polyA_signal
 <222> 814..819

<220>
 <221> polyA_site
 <222> 822..836

<400> 65
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 acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120
 ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaataca tggaaa atg 179
 Met
 aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
 Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
 -20 -15 -10 -5
 gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275
 Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
 1 5 10
 gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg 323
 Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
 15 20 25
 gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371
 Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
 30 35 40
 gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg 419
 Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
 45 50 55 60
 tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa 467
 Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
 65 70 75
 tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg 515
 Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
 80 85 90
 atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc 563
 Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu
 95 100 105
 tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct 611
 Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
 110 115 120
 gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc 659
 Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
 125 130 135 140

act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc 707
 Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
 145 150 155
 cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt 755
 His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
 160 165 170
 ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaaatatg 807
 Phe Ser Pro Ala
 175
 atagtgtata aatgaaaaaa aaaaaaaaaa 836

<210> 66
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..22

<400> 66
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 Leu Ala Ile Leu Ala Ile Leu Thr Arg Trp Ala Arg Arg Lys Gln
 -5 1 5 10
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40
 Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
 60 65 70
 Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala
 75 80 85 90
 Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys
 95 100 105
 Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr
 110 115 120
 Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp
 125 130 135
 Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn
 140 145 150
 Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser
 155 160 165 170
 Leu Phe Ser Pro Ala
 175

<210> 67
 <211> 789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..62

<220>
 <221> CDS

<222> 63..572

<220>

<221> 3'UTR

<222> 573..789

<220>

<221> polyA_signal

<222> 750..755

<220>

<221> polyA_site

<222> 774..789

<400> 67

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ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
20 25 30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
160 165 170
gaggagggac gccagggtg gggaggaaga gtctgcaagc agggctgttg agttaggggtt 652
caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772
gaaaaaaaaa aaaaaaa 789
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<210> 68

<211> 170

<212> PRT

<213> Homo sapiens

<400> 68
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
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Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
20 25 30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35 40 45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50 55 60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65 70 75 80
Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85 90 95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100 105 110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115 120 125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130 135 140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145 150 155 160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165 170

<210> 69
<211> 2556
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..66

<220>
<221> CDS
<222> 67..2427

<220>
<221> 3'UTR
<222> 2428..2556

<220>
<221> polyA_signal
<222> 2522..2527

<220>
<221> polyA_site
<222> 2541..2556

<400> 69
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cgcacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108
Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu
-15 -10 -5
ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156
Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile
1 5 10 15
cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat 204
Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr

Val	Gln	Ser	Asn	Gly	Val	Lys	Thr	Phe	Ser	Ser	Cys	Ser	Leu	Arg	Ser		
				340					345					350			
ttt	caa	aat	ttc	att	tca	aat	gtg	ggt	gtc	aaa	tgt	ctt	cag	aat	aag	1212	
Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys		
			355					360					365				
cca	caa	atg	caa	aaa	aaa	tct	ccg	aaa	cca	gtc	tgt	ggc	aat	ggc	aga	1260	
Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg		
		370					375					380					
ttg	gag	gga	aat	gaa	atc	tgt	gat	tgt	ggt	act	gag	gct	caa	tgt	gga	1308	
Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly		
	385					390					395						
cct	gca	agc	tgt	tgt	gat	ttt	cga	act	tgt	gta	ctg	aaa	gac	gga	gca	1356	
Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala		
400					405					410					415		
aaa	tgt	tat	aaa	gga	ctg	tgc	tgc	aaa	gac	tgt	caa	att	tta	caa	tca	1404	
Lys	Cys	Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser		
			420						425					430			
ggc	gtt	gaa	tgt	agg	ccg	aaa	gca	cat	cct	gaa	tgt	gac	atc	gct	gaa	1452	
Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu		
			435					440					445				
aat	tgt	aat	gga	agc	tca	cca	gaa	tgt	ggt	cct	gac	ata	act	tta	atc	1500	
Asn	Cys	Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile		
		450					455					460					
aat	gga	ctt	tca	tgc	aaa	aat	aat	aag	ttt	att	tgt	tat	gac	gga	gac	1548	
Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp		
	465					470					475						
tgc	cat	gat	ctc	gat	gca	cgt	tgt	gag	agt	gta	ttt	gga	aaa	ggt	tca	1596	
Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser		
480					485					490					495		
aga	aat	gct	cca	ttt	gcc	tgc	tat	gaa	gaa	ata	caa	tct	caa	tca	gac	1644	
Arg	Asn	Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp		
			500						505					510			
aga	ttt	ggg	aac	tgt	ggt	agg	gat	aga	aat	aac	aaa	tat	gtg	ttc	tgt	1692	
Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys		
			515					520					525				
gga	tgg	agg	aat	ctt	ata	tgt	gga	aga	tta	gtt	tgt	acc	tac	cct	act	1740	
Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr		
			530				535					540					
cga	aag	cct	ttc	cat	caa	gaa	aat	ggt	gat	gtg	att	tat	gct	ttc	gta	1788	
Arg	Lys	Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val		
	545				550						555						
cga	gat	tct	gta	tgc	ata	acc	gta	gac	tac	aaa	ttg	cct	cga	aca	gtt	1836	
Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val		
560					565					570					575		
cca	gat	cca	ctg	gct	gtc	aaa	aat	ggc	tct	cag	tgt	gat	att	ggg	agg	1884	
Pro	Asp	Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg		
			580						585					590			
gtt	tgt	gta	aat	cgt	gaa	tgt	gta	gaa	tca	agg	ata	att	aag	gct	tca	1932	
Val	Cys	Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser		
			595					600					605				
gca	cat	gtt	tgt	tca	caa	cag	tgt	tct	gga	cat	gga	gtg	tgt	gat	tcc	1980	
Ala	His	Val	Cys	Ser	Gln	Gln	Cys	Ser	Gly	His	Gly	Val	Cys	Asp	Ser		
		610					615					620					
aga	aac	aag	tgc	cat	tgt	tcg	cca	ggc	tat	aag	cct	cca	aac	tgc	caa	2028	
Arg	Asn	Lys	Cys	His	Cys	Ser	Pro	Gly	Tyr	Lys	Pro	Pro	Pro	Asn	Cys	Gln	
	625					630					635						
ata	cgt	tcc	aaa	gga	ttt	tcc	ata	ttt	cct	gag	gaa	gat	atg	ggg	tca	2076	
Ile	Arg	Ser	Lys	Gly	Phe	Ser	Ile	Phe	Pro	Glu	Glu	Asp	Met	Gly	Ser		
640					645					650					655		

atc atg gaa aga gca tct ggg aag act gaa aac acc tgg ctt cta ggt 2124
 Ile Met Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly
 660 665 670
 ttc ctc att gct ctt cct att ctc att gta aca acc gca ata gtt ttg 2172
 Phe Leu Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu
 675 680 685
 gca agg aaa cag ttg aaa aac tgg ttc gcc aag gaa gag gaa ttc cca 2220
 Ala Arg Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro
 690 695 700
 agt agc gaa tct aaa tcg gaa ggt agc aca cag aca tat gcc agc caa 2268
 Ser Ser Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln
 705 710 715
 tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca 2316
 Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
 720 725 730 735
 gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
 Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
 740 745 750
 gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
 Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
 755 760 765
 caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
 Gln Ser Ser Ser Asn
 770
 tcgctaagaa atgaaaattc tgtcttttcc tccgtgggtca cagctgaaag aaacaataaa 2527
 ttgagtgtgg accaaaaaaa aaaaaaaat 2556

<210> 70
 <211> 787
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..16

<400> 70
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 Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
 1 5 10 15
 Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
 20 25 30
 Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
 35 40 45
 Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn
 50 55 60
 Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
 65 70 75 80
 Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser
 85 90 95
 Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
 100 105 110
 Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His
 115 120 125
 Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
 130 135 140
 Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
 145 150 155 160

Glu	Pro	Ala	Val	Pro	Asp	Leu	Phe	Pro	Leu	Tyr	Leu	Glu	Met	His	Ile
				165					170					175	
Val	Val	Asp	Lys	Thr	Leu	Tyr	Asp	Tyr	Trp	Gly	Ser	Asp	Ser	Met	Ile
			180					185					190		
Val	Thr	Asn	Lys	Val	Ile	Glu	Ile	Val	Gly	Leu	Ala	Asn	Ser	Met	Phe
		195					200					205			
Thr	Gln	Phe	Lys	Val	Thr	Ile	Val	Leu	Ser	Ser	Leu	Glu	Leu	Trp	Ser
	210					215					220				
Asp	Glu	Asn	Lys	Ile	Ser	Thr	Val	Gly	Glu	Ala	Asp	Glu	Leu	Leu	Gln
225					230					235					240
Lys	Phe	Leu	Glu	Trp	Lys	Gln	Ser	Tyr	Leu	Asn	Leu	Arg	Pro	His	Asp
				245					250					255	
Ile	Ala	Tyr	Leu	Leu	Ile	Tyr	Met	Asp	Tyr	Pro	Arg	Tyr	Leu	Gly	Ala
			260					265					270		
Val	Phe	Pro	Gly	Thr	Met	Cys	Ile	Thr	Arg	Tyr	Ser	Ala	Gly	Val	Ala
		275					280					285			
Leu	Tyr	Pro	Lys	Glu	Ile	Thr	Leu	Glu	Ala	Phe	Ala	Val	Ile	Val	Thr
	290					295					300				
Gln	Met	Leu	Ala	Leu	Ser	Leu	Gly	Ile	Ser	Tyr	Asp	Asp	Pro	Lys	Lys
305					310					315					320
Cys	Gln	Cys	Ser	Glu	Ser	Thr	Cys	Ile	Met	Asn	Pro	Glu	Val	Val	Gln
				325						330				335	
Ser	Asn	Gly	Val	Lys	Thr	Phe	Ser	Ser	Cys	Ser	Leu	Arg	Ser	Phe	Gln
			340					345					350		
Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	Pro	Gln
	355					360					365				
Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	Leu	Glu
	370					375					380				
Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly	Pro	Ala
385					390					395					400
Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala	Lys	Cys
				405					410					415	
Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser	Gly	Val
			420					425					430		
Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu	Asn	Cys
		435					440					445			
Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile	Asn	Gly
	450					455					460				
Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp	Cys	His
465					470					475					480
Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser	Arg	Asn
				485					490					495	
Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp	Arg	Phe
			500					505					510		
Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys	Gly	Trp
			515				520						525		
Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr	Arg	Lys
	530					535					540				
Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val	Arg	Asp
545					550					555					560
Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val	Pro	Asp
				565					570					575	
Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg	Val	Cys
			580					585					590		
Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser	Ala	His
			595				600					605			
Val	Cys	Ser	Gln	Gln	Cys	Ser	Gly	His	Gly	Val	Cys	Asp	Ser	Arg	Asn
	610					615					620				
Lys	Cys	His	Cys	Ser	Pro	Gly	Tyr	Lys	Pro	Pro	Asn	Cys	Gln	Ile	Arg

Ala	Ala	Thr	Pro	Ala	Ser	Ala	Ala	Ala	Ala	Thr	Leu	Asp	Val	Ala	Val		
			50					55					60				
cgg	aga	ggc	ctg	tcc	cac	gca	gcc	cag	agg	ctg	ctg	tgc	gtg	gcc	ctg	289	
Arg	Arg	Gly	Leu	Ser	His	Ala	Ala	Gln	Arg	Leu	Leu	Cys	Val	Ala	Leu		
		65					70					75					
gga	cag	ctg	gac	cgg	cct	cca	gac	ctc	gcc	cat	gac	ggg	agg	agt	ctg	337	
Gly	Gln	Leu	Asp	Arg	Pro	Pro	Asp	Leu	Ala	His	Asp	Gly	Arg	Ser	Leu		
		80				85					90						
tgg	ctg	aac	atc	agg	ggc	aag	gag	gcg	gct	gcc	cta	tcc	atg	ttc	cat	385	
Trp	Leu	Asn	Ile	Arg	Gly	Lys	Glu	Ala	Ala	Ala	Leu	Ser	Met	Phe	His		
		95			100				105					110			
gtc	tcc	acg	cca	ctg	cca	gtg	atg	acc	ggt	ggt	ttc	ctg	agc	tgc	atc	433	
Val	Ser	Thr	Pro	Leu	Pro	Val	Met	Thr	Gly	Gly	Phe	Leu	Ser	Cys	Ile		
			115					120						125			
ttg	ggc	ttg	gtg	ctg	ccc	ctg	gcc	tat	ggc	ttc	cag	cct	gac	ctg	gtg	481	
Leu	Gly	Leu	Val	Leu	Pro	Leu	Ala	Tyr	Gly	Phe	Gln	Pro	Asp	Leu	Val		
			130					135					140				
ctg	gtg	gcg	ctg	ggg	cct	ggc	cat	ggc	ctg	cag	ggc	ccc	cac	gst	gca	529	
Leu	Val	Ala	Leu	Gly	Pro	Gly	His	Gly	Leu	Gln	Gly	Pro	His	Xaa	Ala		
		145				150					155						
ctc	ctg	gct	gca	atg	ctt	cgg	ggg	ctg	gca	ggg	ggc	cga	gtc	ctg	gcc	577	
Leu	Leu	Ala	Ala	Met	Leu	Arg	Gly	Leu	Ala	Gly	Gly	Arg	Val	Leu	Ala		
		160				165					170						
ctc	ctg	gag	gag	aac	tcc	aca	ccc	cag	cta	gca	ggg	atc	ctg	gcc	cgg	625	
Leu	Leu	Glu	Glu	Asn	Ser	Thr	Pro	Gln	Leu	Ala	Gly	Ile	Leu	Ala	Arg		
		175			180				185					190			
gtg	ctg	aat	gga	gag	gca	cct	cct	agc	cta	ggc	cct	tcc	tct	gtg	gcc	673	
Val	Leu	Asn	Gly	Glu	Ala	Pro	Pro	Ser	Leu	Gly	Pro	Ser	Ser	Val	Ala		
			195					200					205				
tcc	cca	gag	gac	gtc	cag	gcc	ctg	atg	tac	ctg	aga	ggg	cag	ctg	gag	721	
Ser	Pro	Glu	Asp	Val	Gln	Ala	Leu	Met	Tyr	Leu	Arg	Gly	Gln	Leu	Glu		
		210						215					220				
cct	cag	tgg	aag	atg	ttg	cag	tgc	cat	cct	cac	ctg	gtg	gct			763	
Pro	Gln	Trp	Lys	Met	Leu	Gln	Cys	His	Pro	His	Leu	Val	Ala				
		225				230					235						
tgaaatcggc	caaggtggga	gcatttacac	cgcagaaatg	acaccgcacg	ccagcgcccc	823											
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ccactcccaa	tccccgcgcc	ccgccctctc	ccaccctgac	ttcccccgct	ccaccctca	943											
cctcacctcg	ccccgcggcc	acccatcgcg	ccccggcggc	tggtattgtt	cggctgggct	1003											
cggctggggcg	ctgtctccct	cggctctgcg	ggtgtcagtt	cgtccggctt	cctcacagcc	1063											
cctcactccc	ggcggctgac	agcagcagcg	gcggcggcgg	gcggcgccctg	gcgtttcgag	1123											
getgagcggc	accggggttg	gggcgcggag	gaggagcagc	agcgggagga	ggagccgtgt	1183											
gccctggcac	tgagcggccg	cggccatggc	gtacgcctat	ctcttcaagt	acatcataat	1243											
cggcgacaca	ggtgttggtg	aatcatgctt	attgctacag	tttacagaca	agagggttcag	1303											
ccagtgcattg	accttactat	tggtgttagag	ttcgggtgctc	gaatgataac	tattgatggg	1363											
aaacagataa	aacttcagat	atgggatacg	gcagggcaag	aatcctttcg	ttccatcaca	1423											
aggctcgtatt	acagaggtgc	agcaggagct	ttactagttt	acgatattac	acggagagat	1483											
acattcaacc	acttgacaac	ctgggttagaa	gatgcccgcc	agcattccaa	ttccaacatg	1543											
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<210> 72
 <211> 252
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

<220>
 <221> UNSURE
 <222> 173
 <223> Xaa = Ala,Gly

<400> 72

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1			5						10					15	
Ser	Leu	Ala	Arg	Glu	Glu	Ala	Leu	Thr	Ala	Leu	Gly	Lys	Leu	Leu	Tyr
			20					25					30		
Leu	Leu	Asp	Gly	Met	Leu	Asp	Gly	Gln	Val	Asn	Ser	Gly	Ile	Ala	Ala
			35				40						45		
Thr	Pro	Ala	Ser	Ala	Ala	Ala	Ala	Thr	Leu	Asp	Val	Ala	Val	Arg	Arg
	50						55					60			
Gly	Leu	Ser	His	Ala	Ala	Gln	Arg	Leu	Leu	Cys	Val	Ala	Leu	Gly	Gln
	65					70				75					
Leu	Asp	Arg	Pro	Pro	Asp	Leu	Ala	His	Asp	Gly	Arg	Ser	Leu	Trp	Leu
80					85				90					95	
Asn	Ile	Arg	Gly	Lys	Glu	Ala	Ala	Ala	Leu	Ser	Met	Phe	His	Val	Ser
			100						105					110	
Thr	Pro	Leu	Pro	Val	Met	Thr	Gly	Gly	Phe	Leu	Ser	Cys	Ile	Leu	Gly
			115				120						125		
Leu	Val	Leu	Pro	Leu	Ala	Tyr	Gly	Phe	Gln	Pro	Asp	Leu	Val	Leu	Val
	130						135					140			
Ala	Leu	Gly	Pro	Gly	His	Gly	Leu	Gln	Gly	Pro	His	Xaa	Ala	Leu	Leu
	145					150				155					
Ala	Ala	Met	Leu	Arg	Gly	Leu	Ala	Gly	Gly	Arg	Val	Leu	Ala	Leu	Leu
160					165					170				175	
Glu	Glu	Asn	Ser	Thr	Pro	Gln	Leu	Ala	Gly	Ile	Leu	Ala	Arg	Val	Leu
				180					185					190	
Asn	Gly	Glu	Ala	Pro	Pro	Ser	Leu	Gly	Pro	Ser	Ser	Val	Ala	Ser	Pro
			195					200					205		
Glu	Asp	Val	Gln	Ala	Leu	Met	Tyr	Leu	Arg	Gly	Gln	Leu	Glu	Pro	Gln
	210					215						220			
Trp	Lys	Met	Leu	Gln	Cys	His	Pro	His	Leu	Val	Ala				
	225					230					235				

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 <213> Homo sapiens

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<220>
 <221> CDS
 <222> 9..395

<220>
 <221> 3'UTR
 <222> 396..879

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Pro Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser
1 5 10 15
cca ggg ttc ccc gcc agg ccc ggg agg ggg ccg ccg tac atg gcc agc 146
Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser
20 25 30
agg cct ccg ggg gac ctc gcc gag gct gga ggc cga gct ctg cag agc 194
Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser
35 40 45
tta caa ttg aga ctg cta acc cct acc ttt gaa ggg atc aac gga ttg 242
Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu
50 55 60
ttg ttg aaa caa cat tta gtt cag aat cca gtc aga ctc tgg caa ctt 290
Leu Leu Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu
65 70 75
tta ggt ggt act ttc tat ttt aac acc tca agg ttg aag cag aag aat 338
Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn
80 85 90 95
aag gag aag gat aag tcg aag ggg aag gcg cct gaa gag gac gaa ggt 386
Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly
100 105 110
ata ttc atc tgatgttctt cagtcagtag ctgcctctgg atgtctttac 435
Ile Phe Ile
rtttctgttt wccttttagc aaggtgaaac cagtctggam aatggggaga tgggcccgggt 495
gcagtggctc acacttgtaa tcgaaacgct ttgggaggcc caggtggaag gatcacttga 555
ggcctatacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtgggtggc 615
tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacct gcaccctggc 675
caacatgggtg aaaccccgtc ttactaaaa atagaaaatt agccggggcgt gatggcacac 735
gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggaggtg 795
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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..16

<400> 74
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1 5 10 15
Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
20 25 30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
35 40 45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
50 55 60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
65 70 75 80

Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
 85 90 95
 Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe
 100 105 110
 Ile

<210> 75
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 <213> Homo sapiens

<220>
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 <222> 88..1269

<220>
 <221> 3'UTR
 <222> 1270..1634

<220>
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 <222> 1594..1599

<220>
 <221> polyA_site
 <222> 1619..1634

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 agagtcacgc cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114
 Met Met Gly Val Phe Val Val Ala Ala
 1 5
 aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162
 Lys Arg Thr Pro Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr
 10 15 20 25
 gct act gac ttg tct gaa ttt gct gcc aag gct gcc ttg tct gct ggc 210
 Ala Thr Asp Leu Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly
 30 35 40
 aaa gtc tca cct gaa aca gtt gac agt gtg att atg ggc aat gtc ctg 258
 Lys Val Ser Pro Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu
 45 50 55
 cag agt tct tca gat gct ata tat ttg gca agg cat gtt ggt ttg cgt 306
 Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg His Val Gly Leu Arg
 60 65 70
 gtg gga atc cca aag gag acc cca gct ctc acg att aat agg ctc tgt 354
 Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr Ile Asn Arg Leu Cys
 75 80 85
 ggt tct ggt ttt cag tcc att gtg aat gga tgt cag gaa att tgt gtt 402
 Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys Gln Glu Ile Cys Val
 90 95 100 105
 aaa gaa gct gaa gtt gtt tta tgt gga gga acc gaa agc atg agc caa 450
 Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr Glu Ser Met Ser Gln
 110 115 120
 gct ccc tac tgt gtc aga aat gtg cgt ttt gga acc aag ctt gga tca 498
 Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly Thr Lys Leu Gly Ser

	125		130		135	
gat atc aag ctg gaa gat tct tta tgg gta tca tta aca gat cag cat						546
Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser Leu Thr Asp Gln His						
	140		145		150	
gtc cag ctc ccc atg gca atg act gca gag aat ctt gct gta aaa cac						594
Val Gln Leu Pro Met Ala Met Thr Ala Glu Asn Leu Ala Val Lys His						
	155		160		165	
aaa ata agc aga gaa gaa tgt gac aaa tat gcc ctg cag tca cag cag						642
Lys Ile Ser Arg Glu Glu Cys Asp Lys Tyr Ala Leu Gln Ser Gln Gln						
	170		175		180	185
aga tgg aaa gct gct aat gat gct ggc tac ttt aat gat gaa atg gca						690
Arg Trp Lys Ala Ala Asn Asp Ala Gly Tyr Phe Asn Asp Glu Met Ala						
	190		195		200	
cca att gaa gtg aag aca aag aaa gga aaa cag aca atg cag gta gac						738
Pro Ile Glu Val Lys Thr Lys Lys Gly Lys Gln Thr Met Gln Val Asp						
	205		210		215	
gag cat gct cgg ccc caa acc acc ctg gaa cag tta cag aaa ctt cct						786
Glu His Ala Arg Pro Gln Thr Thr Leu Glu Gln Leu Gln Lys Leu Pro						
	220		225		230	
cca gta ttc aag aaa gat gga act gtt act gca ggg aat gca tcg ggt						834
Pro Val Phe Lys Lys Asp Gly Thr Val Thr Ala Gly Asn Ala Ser Gly						
	235		240		245	
gta gct gat ggt gct gga gct gtt atc ata gct agt gaa gat gct gtt						882
Val Ala Asp Gly Ala Val Ile Ile Ala Ser Glu Asp Ala Val						
	250		255		260	265
aag aaa cat aac ttc aca cca ctg gca aga att gtg ggc tac ttt gta						930
Lys Lys His Asn Phe Thr Pro Leu Ala Arg Ile Val Gly Tyr Phe Val						
	270		275		280	
tct gga tgt gat ccc tct atc atg ggt att ggt cct gtc cct gct atc						978
Ser Gly Cys Asp Pro Ser Ile Met Gly Ile Gly Pro Val Pro Ala Ile						
	285		290		295	
agt ggg gca ctg aag aaa gca gga ctg agt ctt aag gac atg gat ttg						1026
Ser Gly Ala Leu Lys Lys Ala Gly Leu Ser Leu Lys Asp Met Asp Leu						
	300		305		310	
gta gag gtg aat gaa gct ttt gct ccc cag tac ttg gct gtt gag agg						1074
Val Glu Val Asn Glu Ala Phe Ala Pro Gln Tyr Leu Ala Val Glu Arg						
	315		320		325	
agt ttg gat ctt gac ata agt aaa acc aat gtg aat gga gga gcc att						1122
Ser Leu Asp Leu Asp Ile Ser Lys Thr Asn Val Asn Gly Gly Ala Ile						
	330		335		340	345
gct ttg ggt cac cca ctg gga gga tct gga tca aga att act gca cac						1170
Ala Leu Gly His Pro Leu Gly Gly Ser Gly Ser Arg Ile Thr Ala His						
	350		355		360	
ctg gtt cac gaa tta agg cgt cga ggt gga aaa tat gcc gtt gga tca						1218
Leu Val His Glu Leu Arg Arg Arg Gly Gly Lys Tyr Ala Val Gly Ser						
	365		370		375	
gct tgc att gga ggt ggc caa ggt att gct gtc atc att cag agc aca						1266
Ala Cys Ile Gly Gly Gly Gln Gly Ile Ala Val Ile Ile Gln Ser Thr						
	380		385		390	
gcc tgaagagacc agtgagctca ctgtgaccca tccttactct acttggccag						1319
Ala						
gccacagtaa aacaagtgac cttcagagca gctgccacaa ctggccatgc cctgccattg						1379
aaacagtgat taagtttgat caagccatgg tgacacaaaa atgcattgat catgaatagg						1439
agcccatgct agaagtacat tctctcagat ttgaaccagt gaaatatgat gtattttctga						1499
gctaaaactc aactatagaa gacattaaaa gaaatcgtat tcttgccaag taaccaccac						1559
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aaaaaaaaaaaa aaaaa						1634

<210> 76

<211> 394
 <212> PRT
 <213> Homo sapiens

<400> 76

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			20					25				30			
Ala	Ala	Lys	Ala	Ala	Leu	Ser	Ala	Gly	Lys	Val	Ser	Pro	Glu	Thr	Val
		35					40					45			
Asp	Ser	Val	Ile	Met	Gly	Asn	Val	Leu	Gln	Ser	Ser	Ser	Asp	Ala	Ile
	50					55					60				
Tyr	Leu	Ala	Arg	His	Val	Gly	Leu	Arg	Val	Gly	Ile	Pro	Lys	Glu	Thr
65					70					75					80
Pro	Ala	Leu	Thr	Ile	Asn	Arg	Leu	Cys	Gly	Ser	Gly	Phe	Gln	Ser	Ile
				85					90					95	
Val	Asn	Gly	Cys	Gln	Glu	Ile	Cys	Val	Lys	Glu	Ala	Glu	Val	Val	Leu
			100					105					110		
Cys	Gly	Gly	Thr	Glu	Ser	Met	Ser	Gln	Ala	Pro	Tyr	Cys	Val	Arg	Asn
		115					120					125			
Val	Arg	Phe	Gly	Thr	Lys	Leu	Gly	Ser	Asp	Ile	Lys	Leu	Glu	Asp	Ser
	130					135					140				
Leu	Trp	Val	Ser	Leu	Thr	Asp	Gln	His	Val	Gln	Leu	Pro	Met	Ala	Met
145					150					155					160
Thr	Ala	Glu	Asn	Leu	Ala	Val	Lys	His	Lys	Ile	Ser	Arg	Glu	Glu	Cys
				165					170					175	
Asp	Lys	Tyr	Ala	Leu	Gln	Ser	Gln	Gln	Arg	Trp	Lys	Ala	Ala	Asn	Asp
			180					185					190		
Ala	Gly	Tyr	Phe	Asn	Asp	Glu	Met	Ala	Pro	Ile	Glu	Val	Lys	Thr	Lys
		195					200					205			
Lys	Gly	Lys	Gln	Thr	Met	Gln	Val	Asp	Glu	His	Ala	Arg	Pro	Gln	Thr
	210					215					220				
Thr	Leu	Glu	Gln	Leu	Gln	Lys	Leu	Pro	Pro	Val	Phe	Lys	Lys	Asp	Gly
225					230					235					240
Thr	Val	Thr	Ala	Gly	Asn	Ala	Ser	Gly	Val	Ala	Asp	Gly	Ala	Gly	Ala
				245					250					255	
Val	Ile	Ile	Ala	Ser	Glu	Asp	Ala	Val	Lys	Lys	His	Asn	Phe	Thr	Pro
			260					265					270		
Leu	Ala	Arg	Ile	Val	Gly	Tyr	Phe	Val	Ser	Gly	Cys	Asp	Pro	Ser	Ile
		275					280					285			
Met	Gly	Ile	Gly	Pro	Val	Pro	Ala	Ile	Ser	Gly	Ala	Leu	Lys	Lys	Ala
	290					295					300				
Gly	Leu	Ser	Leu	Lys	Asp	Met	Asp	Leu	Val	Glu	Val	Asn	Glu	Ala	Phe
305					310					315					320
Ala	Pro	Gln	Tyr	Leu	Ala	Val	Glu	Arg	Ser	Leu	Asp	Leu	Asp	Ile	Ser
				325					330					335	
Lys	Thr	Asn	Val	Asn	Gly	Gly	Ala	Ile	Ala	Leu	Gly	His	Pro	Leu	Gly
			340				345						350		
Gly	Ser	Gly	Ser	Arg	Ile	Thr	Ala	His	Leu	Val	His	Glu	Leu	Arg	Arg
		355					360					365			
Arg	Gly	Gly	Lys	Tyr	Ala	Val	Gly	Ser	Ala	Cys	Ile	Gly	Gly	Gly	Gln
	370					375					380				
Gly	Ile	Ala	Val	Ile	Ile	Gln	Ser	Thr	Ala						
385					390										

<210> 77
 <211> 1642
 <212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..68

<220>

<221> CDS

<222> 69..875

<220>

<221> 3'UTR

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<220>

<221> polyA_signal

<222> 1599..1604

<220>

<221> polyA_site

<222> 1627..1642

<400> 77

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taggaatc atg gcg gct gcg ctg ttc gtg ctg ctg gga ttc gcg ctg ctg 110
      Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu
      -20              -15              -10
ggc acc cac gga gcc tcc ggg gct gcc ggc aca gtc ttc act acc gta 158
Gly Thr His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val
      -5              1              5              10
gaa gac ctt ggc tcc aag ata ctc ctc acc tgc tcc ttg aat gac agc 206
Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser
      15              20              25
gcc aca gag gtc aca ggg cac cgc tgg ctg aag ggg ggc gtg gtg ctg 254
Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu
      30              35              40
aag gag gac gcg ctg ccc ggc cag aaa acg gag ttc aag gtg gac tcc 302
Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser
      45              50              55
gac gac cag tgg gga gag tac tcc tgc gtc ttc ctc ccc gag ccc atg 350
Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met
      60              65              70
ggc acg gcc aac atc cag ctc cac ggg cct ccc aga gtg aag gcc gtg 398
Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val
      75              80              85              90
aag tcg tca gaa cac atc aac gag ggg gag acg gcc atg ctg gtc tgc 446
Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys
      95              100              105
aag tca gag tcc gtg cca cct gtc act gac tgg gcc tgg tac aag atc 494
Lys Ser Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile
      110              115              120
act gac tct gag gac aag gcc ctc atg aac ggc tcc gag agc agg ttc 542
Thr Asp Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe
      125              130              135
ttc gtg agt tcc tcg cag ggc ctg tca gag cta cac att gag aac ctg 590
Phe Val Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu
      140              145              150
aac atg gag gcc gac ccc ggc cag tac cgg tgc aac ggc acc agc tcc 638
Asn Met Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser
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155          160          165          170
aag ggc tcc gac cag gcc atc atc acg ctc cgc gtg cgc agc cac ctg      686
Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu
          175          180          185
gcc gcc ctc tgg ccc ttc ctg ggc atc gtg gct gag gtg ctg gtg ctg      734
Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu
          190          195          200
gtc acc atc atc ttc atc tac gag aag cgc cgg aag ccc gag gac gtc      782
Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val
          205          210          215
ctg gat gat gac gac gcc ggc tct gca ccc ctg aag agc agc ggg cag      830
Leu Asp Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln
          220          225          230
cac cag aat gac aaa ggc aag aac gtc cgc cag agg aac tct tcc      875
His Gln Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
          235          240          245
tgaggcaggt ggcccgagga cgctccctgc tccgcgtctg cgccgcccgc ggagtccact 935
cccagtgttt gcaagattcc aagttctcac ctcttaaaga aaacccaccc cgtagattcc 995
catcatacac ttcttctttt tttaaaaaag ttgggttttc tccattcagg attctgttcc 1055
ttaggatttt ttcttctga agtgtttcac gagagcccgg gagctgtgc cctgcccggc 1115
cgtctgtggc ttccagcttc tgggtctgag tcatggccgg gtgggcccga cagccttctc 1175
cactggccgg agtcagtgc aggtccttgc cctttgtgga aagtcacagg tcacacgagg 1235
ggccccgtgt cctgcctgtc tgaagccaat gctgtctggt tgcgccattt ttgtgctttt 1295
atgtttaatt ttatgagggc cacgggtctg tgttcgactc agcctcaggg acgactctga 1355
cctcttggcc acagaggact cacttgccca caccgagggc gaccccgta cagcctcaag 1415
tcaactccaa gccccctcct tgtctgtgca tccgggggca gctctggagg gggtttgcctg 1475
gggaactggc gccatcgccg ggactccaga accgcagaag cctccccagc tcacccctgg 1535
aggacggccg gctctctata gcaccagggc tcacgtggga acccccctcc caccaccgc 1595
cacaataaag atcgccccca cctccaccct caaaaaaaaa aaaaaaa 1642

<210> 78
<211> 269
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..21

<400> 78
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-20          -15          -10
His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
-5          1          5          10
Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
          15          20          25
Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
          30          35          40
Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
          45          50          55
Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
60          65          70          75
Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser
          80          85          90
Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
          95          100          105
Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
          110          115          120
Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val

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125		130		135	
Ser Ser Ser Gln Gly	Leu Ser Glu Leu His Ile	Glu Asn Leu Asn Met			
140	145	150	155		
Glu Ala Asp Pro Gly	Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly				
	160	165	170		
Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala					
	175	180	185		
Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr					
	190	195	200		
Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp					
	205	210	215		
Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln					
220	225	230	235		
Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser					
	240	245			

<210> 79
 <211> 1466
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..343

<220>
 <221> CDS
 <222> 344..1144

<220>
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 <222> 1145..1466

<400> 79
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 aattggcagc cttagaacta gtgggaaggc ggggtgcgcga agtcgagggg cggagagagg 120
 gggccggagg agctgcttgc tgaatccaag ttcgtgggct ctctcagaag tcctcaggac 180
 ggagcagagg tggccggcgg gcccggetga ctgcgcctyt gctttctttc cataaccttt 240
 tctttcggac tcgaatcacg gctgctgcga aggggtctagt tccggacact aggggtgcccg 300
 aacgcgctga tgccccgagt gctcgcaggg cttcccgcta acc atg ctg ccg ccg 355
 Met Leu Pro Pro
 ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg 403
 Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu Leu
 -25 -20 -15 -10
 gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca tcc cca ggc cca 451
 Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro
 -5 1 5
 gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg gag ggc gag ggc 499
 Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly
 10 15 20
 tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg cgg ggc tgc ctg 547
 Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro Arg Gly Cys Leu
 25 30 35
 gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg gaa tgc gcc aac 595
 Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp Glu Cys Ala Asn
 40 45 50 55
 ctc gag ggc cag ctc tgc gac ctg gac ccc agt gct cac ttc tac ggg 643
 Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala His Phe Tyr Gly
 60 65 70

cac tgc ggc gag cag ctt gag tgc cgg ctg gac aca ggc ggc gac ctg 691
His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr Gly Gly Asp Leu
75 80 85
agc cgc gga gag gtg ccg gaa cct ctg tgt gcc tgt cgt tgc cag agt 739
Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys Arg Ser Gln Ser
90 95 100
ccg ctc tgc ggg tcc gac ggt cac acc tac tcc cag atc tgc cgc ctg 787
Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln Ile Cys Arg Leu
105 110 115
cag gag gcg gcc cgc gct cgg ccc gat gcc aac ctc act gtg gca cac 835
Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu Thr Val Ala His
120 125 130 135
ccg ggg ccc tgc gaa tgc ggg ccc cag atc gtg tca cat cca tat gac 883
Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser His Pro Tyr Asp
140 145 150
act tgg aat gtg aca ggg cag gat gtg atc ttt ggc tgt gaa gtg ttt 931
Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly Cys Glu Val Phe
155 160 165
gcc tac ccc atg gcc tcc atc gag tgg agg aag gat ggc ttg gac atc 979
Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu Asp Ile
170 175 180
cag ctg cca ggg gat gac ccc cac atc tct gtg cag ttt agg ggt gga 1027
Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg Gly Gly
185 190 195
ccc cag agg ttt gag gtg act ggc tgg ctg cag atc cag gct gtg cgt 1075
Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala Val Arg
200 205 210 215
ccc agt gat gag ggc act tac cgc tgc ctt ggc cca atg ccc tgg gtc 1123
Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro Met Pro Trp Val
220 225 230
aag tgg agg ccc ctg cta gct tgacagtgtt cacacctgac cagctgaact 1174
Lys Trp Arg Pro Leu Leu Ala
235
ctacaggcat cccccagctg cgatcactaa acctgggttcc tgaggaggag gctgagagtg 1234
aagagaatga cgattactac taggtccaga gctctggccc atgggggtgg gtgagcggct 1294
atagtgttca tccctgctct tgaaaagacc tggaaagggg agcaggggtcc cttcatcgac 1354
tgctttcatg ctgtcagtag ggatgatcat gggaggccta tttgactcca aggtagcagt 1414
gtggtaggat agagacaaaa gctggaggag ggtagggaga gaagctgaga cc 1466

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<211> 267
<212> PRT
<213> Homo sapiens

<220>
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<222> 1..30

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Leu Leu Leu Leu Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro
-10 -5 1
Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala
5 10 15
Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro
20 25 30
Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp
35 40 45 50

Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala
 55 60 65
 His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr
 70 75 80
 Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys
 85 90 95
 Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln
 100 105 110
 Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
 115 120 125 130
 Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
 135 140 145
 His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
 150 155 160
 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
 165 170 175
 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
 180 185 190
 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
 195 200 205 210
 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro
 215 220 225
 Met Pro Trp Val Lys Trp Arg Pro Leu Leu Ala
 230 235

<210> 81
 <211> 1406
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..26

<220>
 <221> CDS
 <222> 27..689

<220>
 <221> 3'UTR
 <222> 690..1406

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 <222> 1302..1307

<220>
 <221> polyA_site
 <222> 1325..1406

<400> 81
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 Met Ala Gly Gly Val Arg Pro Leu Arg
 -30 -25
 ggc ctc cgc gcc ttg tgt cgc gtg ctg ctc ttc ctt tcg cag ttc tgc 101
 Gly Leu Arg Ala Leu Cys Arg Val Leu Leu Phe Leu Ser Gln Phe Cys
 -20 -15 -10
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 Ile Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys

-5	1	5	10	
tgt ccg agc aat ggt ttg tgt agc agg ctt cct gca gac tgt ata gac				197
Cys Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp				
15	20	25		
tgc aca aca aat ttc tcc tgt acc tat ggg aag cct gtc act ttt gac				245
Cys Thr Thr Asn Phe Ser Cys Thr Tyr Gly Lys Pro Val Thr Phe Asp				
30	35	40		
tgt gca gtg aaa cca tct gtt acc tgt gtt gat caa gac ttc aaa tcc				293
Cys Ala Val Lys Pro Ser Val Thr Cys Val Asp Gln Asp Phe Lys Ser				
45	50	55		
caa aag aac ttc atc att aac atg act tgc aga ttt tgc tgg cag ctt				341
Gln Lys Asn Phe Ile Ile Asn Met Thr Cys Arg Phe Cys Trp Gln Leu				
60	65	70		
cct gaa aca gat tac gag tgt acc aac tcc acc agc tgc atg acg gtg				389
Pro Glu Thr Asp Tyr Glu Cys Thr Asn Ser Thr Ser Cys Met Thr Val				
75	80	85	90	
tcc tgt cct cgg cag cgc tac cct gcc aac tgc acg gtg cgg gac cac				437
Ser Cys Pro Arg Gln Arg Tyr Pro Ala Asn Cys Thr Val Arg Asp His				
95	100	105		
gtc cac tgc ttg ggt aac cgt act ttt ccc aaa atg cta tat tgc aat				485
Val His Cys Leu Gly Asn Arg Thr Phe Pro Lys Met Leu Tyr Cys Asn				
110	115	120		
tgg act gga ggc tat aag tgg tct acg gct ctg gct cta agc atc acc				533
Trp Thr Gly Tyr Lys Trp Ser Thr Ala Leu Ala Leu Ser Ile Thr				
125	130	135		
ctc ggt ggg ttt gga gca gac cgt ttc tac ctg ggc cag tgg cgg gaa				581
Leu Gly Gly Phe Gly Ala Asp Arg Phe Tyr Leu Gly Gln Trp Arg Glu				
140	145	150		
ggc ctc ggc aag ctc ttc agc ttc ggt ggc ctg gga ata tgg acg ctg				629
Gly Leu Gly Lys Leu Phe Ser Phe Gly Gly Leu Gly Ile Trp Thr Leu				
155	160	165	170	
ata gac gtc ctg ctc att gga gtt ggc tat gtt gga cca gca gat ggc				677
Ile Asp Val Leu Leu Ile Gly Val Gly Tyr Val Gly Pro Ala Asp Gly				
175	180	185		
tct ttg tac att tagctgtggt gtgtgcttca gaaaggagca gggcttagaa				729
Ser Leu Tyr Ile				
190				
aaagcccttt tgtccgtagg agttgatgtg gtgtgagtga tatatttcta tgtttttaat				789
gtacagcacc tgtactttgt ttgccttgat aaaggtaaga taaatgaaac gctgaactat				849
gctaactctgg aatttgtttt tatttgccctg aaatatattt ttttctgtga aaaaattaaa				909
acgtacttaa gccaggagaa tgaattatac agtgattgaa aatccattta attcctatga				969
cttttgtttt gtattgcca agtcaaacta catcacttgt atctccagcc caaatgtagt				1029
ctgccttgaa aagtctttca gctgtgactg caggaagtgg gagtggtttt attgttagct				1089
aattgctgtg actgcaggaa gtgggagtgt ttctgttgtt ggctaattga agttattagg				1149
ctcagcttca gtcattgtgta agttttgcag tgtaatacat atgtagtctg gtctgtatat				1209
atgaaaattt gaattaaact gcagaatgtt tatgtctagt tatggtttaa attttcttag				1269
tagtatataa aaggtaagag tactgaaaaa ttaataaaat tgcaagttaa gaaataaaaa				1329
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taaaaaaaaa aaaaaaat				1406

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 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..32

<400> 82
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-30 -25 -20
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-15 -10 -5
Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
1 5 10 15
Ser Arg Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys
20 25 30
Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val
35 40 45
Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn
50 55 60
Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys
65 70 75 80
Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr
85 90 95
Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg
100 105 110
Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp
115 120 125
Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp
130 135 140
Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser
145 150 155 160
Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly
165 170 175
Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile
180 185

<210> 83
<211> 1754
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..117

<220>
<221> CDS
<222> 118..510

<220>
<221> 3'UTR
<222> 511..1754

<220>
<221> polyA_signal
<222> 1718..1723

<220>
<221> polyA_site
<222> 1739..1754

<400> 83
tccccggccg ccgccgttgc gctcgccgcg ctcgactga agccccgggccc ctcgcgcgccc 60
gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165

Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100 105
 ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc 550
 Gly Pro Ser
 acagacattc gggagacggc ctctgtgttc gccatcaactg cggccggcgc cagccacgcc 610
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
 cgggccccctc cccggccctc cggcctgccc ggcacccccg gaccccttg ccccgcgggc 730
 tccccggaag gcagcgccgc ctgggagtg gagggtgcg gcgacgacgt ggacttcggg 790
 gacgagaagt cgaggetctt tatgsacgcg cggcacaagc ggggacgcgg agacatccgc 850
 gcgttggtgc aactgcacaa caacgagggc ggcaggctgg ccgtgcggag ccacacgcgc 910
 accagtgca aatgccacgg gctgtcgga tcatgcgcgc tgcgcacctg ctggcagaag 970
 ctgcctccat ttcgcgaggt gggcgcgcg cgtgtggagc gcttccacgg cgcctcacgc 1030
 gtcattgggca ccaacgacgg caaggccctg ctgcccgcg tccgcacgct caagccgccc 1090
 ggccgagcgg acctcctcta cgcgcgcgat tgcgccgact tctgcgcccc caaccgacgc 1150
 accggctccc ccggcacgcg cggctcgcgc tgcaatagca gcgccccgga cctcagcggc 1210
 tgccacctgc tgtgtgcgg ccgcgggcac cgccaggaga gcgtgcagct cgaagagaac 1270
 tgccctgtgc gcttccactg gtgctgcgta gtacagtgcc accgctgccg tgtgcgcaag 1330
 gagctcagcc tctgcctgtg acccgccgcc cggccgctag actgacttcg cgcagcgggtg 1390
 gctcgcacct gtgggacctc agggcacccg caccgggcgc ctctcgccgc tcgagcccag 1450
 cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
 aggaacgccc acccacgaag gccaggggc ccgacggccc ccgaaaaggc gctcggggag 1570
 cgtttaaagg aactgtaca ggccctccct ccccttggcc tctaggagga aacagttttt 1630
 tagactggaa aaaagccagt cttaaaggcct ctggatactg ggctccccag aactgctggc 1690
 cacaggatgg tgggtgaggt tagtatcaat aaagatatatt aaaccaccaa aaaaaaaaaa 1750
 aaaa 1754

<210> 84
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 84
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
 -20 -15 -10

Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 25 30 35 40
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100
 Gly Pro Ser
 105

<210> 85
 <211> 1754
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..117

<220>
 <221> CDS
 <222> 118..510
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 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

<400> 85
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 gcgggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct ccg ggc gcc ccg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe


```

      45      50      55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc      405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60      65      70
atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg      453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
      75      80      85
cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca      501
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
      90      95      100      105
ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc      550
Gly Pro Ser
acagacattc gggagacggc cttcgtgttc gccatcactg cggccggcgc cagccacgcc 610
gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
cgggccccctc ccggccctc cggcctgccc ggcacccccg gacccccctg ccccgcgggc 730
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gacgagaagt cgaggctctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850
gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910
accgagtgc aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970
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aggaacgccc acccacgaag gccccagggc ccagacggcc ccgaaaaggc gctcggggag 1570
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aaaa
1754

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<210> 86
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

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<400> 86
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      -20      -15      -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5      1      5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
      10      15      20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      25      30      35      40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45      50      55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60      65      70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
      75      80      85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro

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90
Gly Pro Ser
105

95

100

<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..151

<220>
<221> CDS
<222> 152..655

<220>
<221> 3'UTR
<222> 656..1431

<220>
<221> polyA_signal
<222> 1399..1404

<220>
<221> polyA_site
<222> 1416..1431

<400> 87

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gcccaaacca aggccccag agaggtcccc caggcccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
                               Met Leu Phe Arg Leu Ser Glu
                               1           5

cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
      10           15           20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
      25           30           35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
      40           45           50           55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
      60           65           70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
      75           80           85
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
      90           95           100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
      105           110           115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
      120           125           130           135

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tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta	604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu	
140 145 150	
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc	652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly	
155 160 165	
aca taggcaccca gcctgcatct cccaggagga agtggagggg acatcgctgt	705
Thr	
tccccagaaa cccactctat cctcaccctg ttttgtgtctc ttcccctcgc ctgctagggc	765
tgcggtttct gacttctaga agactaaggc tggctctgtgt ttgcttggtt gccacacctt	825
ggctgatacc cagagaacct gggcacttgc tgcctgatgc ccaccctgc cagtcattcc	885
tccattcacc cagcgggagg tgggatgtga gacagccac attggaaaat ccagaaaacc	945
gggaacaggg atttgccctt cacaattcta ctcccagat cctctcccct ggacacagga	1005
gaccacaggg gcaggacct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc	1065
cttagatcct tttctaccca ctttctatg gaggattcca agtcaccact tctctaccg	1125
gcttctacca ggggtccagga ctaaggcgtt tttctccata gcctcaacat tttgggaatc	1185
ttcccttaat cacccttgtt cctcctgggt gcctggaaga tggactggca gagacctctt	1245
tggtgcgttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac	1305
acagcggggg gcgccaggtt ttccttgtcc cccagctgct ctgccccctt ccccttcttc	1365
cctgactcca ggcctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa	1425
aaaaaa	1431

<210> 88
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 88
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1 5 10 15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
20 25 30
Pro Asn Pro Cys Ala Tyr Thr Pro Ser Leu Lys Ala Val Gln Arg
35 40 45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
50 55 60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65 70 75 80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
85 90 95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
100 105 110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
115 120 125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
130 135 140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145 150 155 160
Pro Ser Pro Ser Glu Pro Gly Thr
165

<210> 89
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..151

<220>
 <221> CDS
 <222> 152..655

<220>
 <221> 3'UTR
 <222> 656..1431

<220>
 <221> polyA_signal
 <222> 1399..1404

<220>
 <221> polyA_site
 <222> 1416..1431

<400> 89
 aatttttttct cacaaggact ggggtgaagag ttctgcagcc ttacagagac tggaaaagaa 60
 gccccaaacca agggccccag agagggtcccc caggccccctt tgggtccctg agcctcagct 120
 ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
 Met Leu Phe Arg Leu Ser Glu
 1 5
 cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
 His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
 10 15 20
 gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
 Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
 25 30 35
 cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
 Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
 40 45 50 55
 tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
 Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
 60 65 70
 ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
 Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
 75 80 85
 gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
 Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
 90 95 100
 gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
 Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
 105 110 115
 ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
 Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
 120 125 130 135
 tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
 Ser Glu Arg Asp Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
 140 145 150
 agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
 Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
 155 160 165
 aca taggcacca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
 Thr
 tccccagaaa ccactctat cctcaccttg ttttgtgtc ttcccctcgc ctgctagggc 765
 tgcggcttct gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccaccttt 825
 ggctgatacc cagagaacct gggcacttgc tgctgatgc ccaccctgc cagtcattcc 885
 tccattcacc cagcgggagg tgggatgtga gacagccac attggaaaat ccagaaaacc 945

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gggaacaggg atttgccctt cacaattcta ctcccagat cctctcccct ggacacagga 1005
gaccacaggg gcaggaccct aagatctggg gaaaggagggt cctgagaacc ttgaggtacc 1065
cttagatcct tttctaccca ctttcctatg gaggattcca agtcaccact tctctcaccg 1125
gcttctacca ggggtccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185
ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tgttgcggtt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccagggt ttccttgctc ccagctgct ctgccccctt ccccttcttc 1365
cctgactcca ggcctgaacc cctcccgctg tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa                                     1431

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<210> 90
<211> 168
<212> PRT
<213> Homo sapiens

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<400> 90
Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
1          5          10          15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
          20          25          30
Pro Asn Pro Cys Ala Tyr Thr Pro Ser Leu Lys Ala Val Gln Arg
          35          40          45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
          50          55          60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65          70          75          80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
          85          90          95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
          100          105          110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
          115          120          125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
          130          135          140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
          145          150          155          160
Pro Ser Pro Ser Glu Pro Gly Thr
          165

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<210> 91
<211> 1417
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..47

<220>
<221> CDS
<222> 48..1301

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<220>
<221> 3'UTR
<222> 1302..1417

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<220>
<221> polyA_signal
<222> 1360..1365

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<220>
 <221> polyA_site
 <222> 1402..1417

<400> 91

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                                     Met Pro Ser

tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc      104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20                                     -15      -10      -5
cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca      152
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
                                     1      5      10
gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc      200
Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
                                     15      20      25
ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac      248
Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
                                     30      35      40
cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca      296
Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
45                                     50      55      60
gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa      344
Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
                                     65      70      75
atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag      392
Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
80                                     85      90
atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac      440
Ile His Glu Gly Phe Gln Glu Leu Arg Thr Leu Asn Gln Pro Asp
95                                     100      105
agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc      488
Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
110      115      120
ctg aag cta gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac      536
Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
125      130      135      140
tca gaa gcc ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa      584
Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
145      150      155
cag atc aac gat tac gtg gag aag ggt act caa ggg aaa att gtg gat      632
Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp
160      165      170
ttg gtc aag gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac      680
Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr
175      180      185
atc ttc ttt aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc      728
Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr
190      195      200
gag gaa gag gac ttc cac gtg gac cag gcg acc acc gtg aag gtg cct      776
Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val Lys Val Pro
205      210      215      220
atg atg aag cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg      824
Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu
225      230      235
tcc agc tgg gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc      872
Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile
240      245      250

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ttc ttc ctg cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc 920
Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu
255 260 265
acc cac gat atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct 968
Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser
270 275 280
gcc agc tta cat tta ccc aaa ctg tcc att act gga acc tat gat ctg 1016
Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu
285 290 295 300
aag agc gtc ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg 1064
Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly
305 310 315
gct gac ctc tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag 1112
Ala Asp Leu Ser Gly Val Thr Glu Ala Pro Leu Lys Leu Ser Lys
320 325 330
gcc gtg cat aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct 1160
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala
335 340 345
gct ggg gcc atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag 1208
Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu
350 355 360
gtc aag ttc aac aaa ccc ttt gtc ttc tta atg att gaa caa aat acc 1256
Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr
365 370 375 380
aag tct ccc ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa 1301
Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys
385 390 395
taactgcctc tcgctcctca acccctcccc tccatccctg gccccctccc tggatgacat 1361
taaagaaggg ttgagctggt cctgcctgc atgtgactgc aaaaaaaaaa aaaaaa 1417

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<210> 92
 <211> 418
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

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<400> 92
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-20 -15 -10
Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
-5 1 5
Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
10 15 20
Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
25 30 35 40
Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
45 50 55
Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
60 65 70
His Asp Glu Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro
75 80 85
Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
90 95 100
Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
105 110 115 120
Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys

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<400> 93
ctcttttgctc taacagacag cagcgacttt aggetggata atagtcaa at tcttacctcg 60
ctcttttcaact gctagtaaga tcagattgcg tttcttttcag ttactcttca atcgccagtt 120
tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
Met His Phe Gly Leu Leu
-15
tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
-10 -5 1
gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
5 10 15 20
aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
25 30 35
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
40 45 50
gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
55 60 65
agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
70 75 80
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
85 90 95 100
gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
105 110 115
aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
120 125 130
gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggt 783
Ala Ile
ccgaatggtt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843
actccgcaat caaccaaggt tcccagcctt tttgttacaa aagaaggaaac aaatgatggt 903
tggaagaatg cggtcatat ttaccaagtc tttctgaacg ccttctgcat tcatgcatcc 963
atgttctttc taggattgga tagcatttca tgcctatggt aatatttgtg cttttggcat 1023
ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
atattttacat gcataggaaa aaaaaaaaaa aa 1115

<210> 94
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..19

<400> 94
Met His Phe Gly Leu Leu Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro
-15 -10 -5
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
1 5 10

cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga 483
Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg
35 40 45 50
cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga 531
Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg
55 60 65
ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca 579
Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala
70 75 80
aac agg att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc 627
Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys
85 90 95
ttt ttg gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat 675
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
100 105 110
ttt tat aac aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga 723
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
115 120 125 130
tgc ctg ggc aat caa caa ttt tgagacactg gaacaatgca agaacatttg 774
Cys Leu Gly Asn Gln Phe
135
tgaagatggg ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa 834
taactccctg actccgcaat caaccaaggt tcccagcctt tttgaatttc acgggtccctc 894
atggtgtctc actccagcag acagaggatt gtgtcgtgcc aatgagaaca gattctacta 954
caattcagtc attgggaaat gccgcccatt taagtacagt ggatgtgggg gaaatgaaaa 1014
caattttact tccaaacaag aatgtctgag ggcattgtaa aaagggtttca tccaaagaat 1074
atcaaaagga ggcctaatta aaaccaaag aaaaagaaag aagcagagag tgaaaatagc 1134
atatgaagaa atttttgtta aaaatatgtg aattttgttat agcaatgtaa cattaattct 1194
actaaatatt ttatatgaaa tgtttcacta tgattttcta tttttcttct aaaatgcttt 1254
taattaatat gttcattaaa ttttctatgc ttattgcaaa aaaaaaaaaa aaa 1307

<210> 96
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..28

<400> 96
Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
-25 -20 -15
Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
-10 -5 1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5 10 15 20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
25 30 35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
40 45 50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
55 60 65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile
70 75 80
Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu
85 90 95 100
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
105 110 115

Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
120 125 130

Asn Gln Gln Phe
135

<210> 97
<211> 1855
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..117

<220>
<221> CDS
<222> 118..504

<220>
<221> 3'UTR
<222> 505..1855

<220>
<221> polyA_signal
<222> 1819..1824

<220>
<221> polyA_site
<222> 1840..1855

<400> 97
tccccggccg ccgcccgttgc gctcgccgcg ctgcactga agccccgggcc ctgcgcgcgcc 60
gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
-20 -15 -10
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
75 80 85
tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90 95 100 105
gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554
Ala

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cctcccaggc ccctggggca gccctcccgc cgcaggtttc aggtcccagg ccccagctga 614
ccgccccagc ccgcgctgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
cgtgttcgcc atcactgcgg ccggcgccag ccacgccgtc acgcaggcct gttctatggg 734
cgagctgctg cagtgcgggt gccaggcgcc ccgcggggcg gcccctcccc ggccctccgg 794
cctgccccgc acccccggac ccctggccc cgcggggtcc ccggaaggca gcgccgcctg 854
ggagtgggga ggctgcggcg acgacgtgga cttcggggac gagaagtcga ggctctttat 914
ggacgcgcgg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974
cgaggcgggc aggttgcccg tgcggagcca cacgcgcacc gagtgcaaat gccacgggct 1034
gtcgggatca tgcgcgtgc gcacctgtg gcagaagctg cctccatttc gcgagggtggg 1094
cgcgcggtc ctggagcgt tccacggcg ctcacgcgtc atgggcacca acgacggcaa 1154
ggccctgctg cccgccgtcc gcacgtcaa gccgcggggc cgagcggacc tcctctacgc 1214
cgccgattcg cccgacttct gcgccccaa ccgacgcacc ggctcccccg gcacgcgcgg 1274
tcgcgcctgc aatagcagcg ccccgaccct cagcggctgc gacctgctgt gctgcggccg 1334
cgggcaccgc caggagagcg tgcagctcga agagaactgc ctgtgccgt tccactgggtg 1394
ctgcgtagta cagtgccacc gctgccgtgt gcgcaaggag ctcagcctct gcctgtgacc 1454
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gcaccggcac cgggcgcctc tcgccgctcg agcccagcct ctccctgcca aagcccaact 1574
cccagggtc tggaaatggt gaggcgaggg gcttgagagg aacgcccacc cacgaaggcc 1634
cagggcgcca gacggccccg aaaaggcgct cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctccc ctggcctct aggaggaaac agtttttttag actggaaaaa agccagtcta 1754
aaggcctctg gatactgggc tccccagaac tgctggccac aggatggtgg gtgaggttag 1814
tatcaataaa gatatttaaa ccaccaaaaa aaaaaaaaaa a 1855

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<210> 98
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
          -20          -15          -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
    10          15          20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
          75          80          85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
    90          95          100
Ala
105

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<210> 99
<211> 667
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR

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<222> 1..94

<220>

<221> CDS

<222> 95..613

<220>

<221> 3'UTR

<222> 614..667

<220>

<221> polyA_signal

<222> 636..641

<220>

<221> polyA_site

<222> 652..667

<400> 99

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ctctgcaaat ccaggacaca cattgtgctc cgcgctccac taaaggcttg agtgggcact 60
gttccatctc aacagcccct gttttggaaa ggac atg att gtc aag ggg gtg gcc 115
Met Ile Val Lys Gly Val Ala
1 5
tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163
Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser
10 15 20
tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val
25 30 35
gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259
Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile
40 45 50 55
ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys
60 65 70
acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile
75 80 85
aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr
90 95 100
gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
105 110 115
tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met
120 125 130 135
gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val
140 145 150
gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys
155 160 165
caa acc act gtg aaa aat tagctttgaa agctatatct ggaataaata 643
Gln Thr Thr Val Lys Asn
170
tctttcgcaa aaaaaaaaaa aaaa 667
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<210> 100

<211> 173
 <212> PRT
 <213> Homo sapiens

<400> 100
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 1 5 10 15
 Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly
 20 25 30
 Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn
 35 40 45
 Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val
 50 55 60
 Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile
 65 70 75 80
 His Gly Tyr Ala Phe Ala Ile Thr Asn Asn Gly Tyr Ile Leu Thr His
 85 90 95
 Pro Glu Leu Arg Leu Leu Tyr Glu Glu Gly Lys Lys Arg Arg Lys Pro
 100 105 110
 Asn Tyr Ser Ser Val Asp Leu Ser Glu Val Glu Trp Glu Asp Arg Asp
 115 120 125
 Asp Val Leu Arg Asn Ala Met Val Asn Arg Lys Thr Gly Lys Phe Ser
 130 135 140
 Met Glu Val Lys Lys Thr Val Asp Lys Gly Val His Phe Ser Gln Thr
 145 150 155 160
 Phe Leu Leu Leu Asn Leu Lys Gln Thr Thr Val Lys Asn
 165 170

<210> 101
 <211> 1062
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..153

<220>
 <221> CDS
 <222> 154..639

<220>
 <221> 3'UTR
 <222> 640..1062

<220>
 <221> polyA_signal
 <222> 1023..1028

<220>
 <221> polyA_site
 <222> 1047..1062

<400> 101
 attggtgtat ggctttgcag caataactga tggctgtttc cctcctgct ttatctttca 60
 gttaatgacc agccacggcg tccctgctgt gagctctggc cgctgccttc cagggctccc 120
 gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg 174
 Met Ala Cys Trp Pro Gln Leu
 1 5

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agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt 222
Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys
10 15 20
cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg 270
Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu
25 30 35
atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat 318
Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His
40 45 50 55
ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag 366
Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln
60 65 70
ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro
75 80 85
ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct 462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala
90 95 100
cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac 510
Arg Leu Phe Ser Asp Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp
105 110 115
acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc 558
Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile
120 125 130 135
aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag 606
Lys Lys Ser Ser Ser Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln
140 145 150
aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtcct cattgtcagg 659
Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu
155 160
cctctaagcc caagccaagc catcgcaccc cctgtgactt gcacatatat gccagatgg 719
cctgaagtaa ctgaagaatc acaaaagaag tgaaaaggcc ctgcctcgcc ttaactgatg 779
acgttcacc attgtgattt gttcctgccc cacccttaact gaggatgattaa cctgtggaat 839
ttccttctcc tggctcagaa gctccccac tgagcacctt gtgacccct gccctgccc 899
accagagaac aacccccctt gactgtaatt ttccattacc ttcccaaata ctataaaaacg 959
gccccacccc tatctccctt tgctgactct cttttcggac tcagcccacc tgcagccagg 1019
tgaaaaaaac agctttattg ctcacacaaa aaaaaaaaaa aaa 1062

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<210> 102

<211> 162

<212> PRT

<213> Homo sapiens

<400> 102

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Met Ala Cys Trp Pro Gln Leu Arg Leu Leu Leu Trp Lys Asn Leu Thr
1 5 10 15
Phe Arg Arg Arg Gln Thr Cys Gln Leu Leu Leu Glu Val Ala Trp Pro
20 25 30
Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
35 40 45
Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
50 55 60
Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
65 70 75 80
Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
85 90 95
Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
100 105 110
Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val

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115 120 125
 Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys
 130 135 140
 Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala
 145 150 155 160
 Leu Leu

<210> 103
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..149

<220>
 <221> CDS
 <222> 150..392

<220>
 <221> 3'UTR
 <222> 393..933

<220>
 <221> polyA_site
 <222> 63..933

<400> 103
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 ggaaaaaaaaaaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120
 cagatgtgta.cggatgaaaa tacagtgag atg agt cag aaa ccg gcc aag gag 173
 Met Ser Gln Lys Pro Ala Lys Glu
 1 5
 ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
 Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
 10 15 20
 cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
 His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
 25 30 35 40
 gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
 Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
 45 50 55
 gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
 Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
 60 65 70
 aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412
 Lys Ile Arg Pro Thr Pro Lys Lys Lys
 75 80
 ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac ccttggatga 472
 agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
 gctcatgggc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592
 tcatccatt gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
 atccttccac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
 tggaaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
 gcgtgggtggc gggcgctgt ggtcccagct actcgggagg ctgaggcagg agaatggcgt 832
 gaacctggga ggcggagctt gcagtgaagg gagatcgcac cactgcactc cagcctgggc 892
 gacagagcga gactctgtct caaacaaaaa aaaaaaaaaa a 933

<210> 104
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Ser Gln Lys Pro Ala Lys Glu Gly Pro Arg Leu Ser Lys Asn Gln
 1 5 10 15
 Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
 20 25 30
 Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
 35 40 45
 Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala
 50 55 60
 Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
 65 70 75 80
 Lys

<210> 105
 <211> 1187
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..34

<220>
 <221> CDS
 <222> 35..1069

<220>
 <221> 3'UTR
 <222> 1070..1187

<220>
 <221> polyA_signal
 <222> 1146..1151

<220>
 <221> polyA_site
 <222> 1172..1187

<400> 105
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 Met Ile Ser Pro Val Leu Ile
 -15
 ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt 103
 Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys
 -10 -5 1 5
 ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca 151
 Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr
 10 15 20
 ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat 199
 Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr
 25 30 35
 gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg 247
 Val Ser Arg Gly Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu
 40 45 50

tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct	295
Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala	
55 60 65	
gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc	343
Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro	
70 75 80 85	
aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct	391
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala	
90 95 100	
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct	439
Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro	
105 110 115	
gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca	487
Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala	
120 125 130	
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg	535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg	
135 140 145	
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat	583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn	
150 155 160 165	
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa	631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu	
170 175 180	
tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt	679
Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe	
185 190 195	
gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gcc aca	727
Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr	
200 205 210	
ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa	775
Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu	
215 220 225	
tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct	823
Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser	
230 235 240 245	
tgt aaa gta cct gtg aaa aaa gcc act gtg gtg tac caa gga gag aga	871
Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg	
250 255 260	
gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa	919
Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys	
265 270 275	
gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag	967
Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu	
280 285 290	
gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag	1015
Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys	
295 300 305	
gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag	1063
Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys	
310 315 320 325	
cca tgc taaggtggtt ttcagattcc acataaaatg tcacacttgt ttcttggtca	1119
Pro Cys	
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aaaaaaaa	1187

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<213> Homo sapiens

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<221> SIGNAL

<222> 1..19

<400> 106

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			1				5					10			
Thr	Val	Val	Pro	Leu	Lys	Thr	Phe	Tyr	Glu	Pro	Gly	Glu	Glu	Ile	Thr
	15					20					25				
Tyr	Ser	Cys	Lys	Pro	Gly	Tyr	Val	Ser	Arg	Gly	Gly	Met	Arg	Lys	Phe
30					35					40					45
Ile	Cys	Pro	Leu	Thr	Gly	Leu	Trp	Leu	Ile	Asn	Thr	Leu	Lys	Cys	Thr
				50					55					60	
Pro	Arg	Val	Cys	Pro	Phe	Ala	Gly	Ile	Leu	Glu	Asn	Gly	Ala	Val	Arg
			65				70						75		
Tyr	Thr	Thr	Phe	Glu	Tyr	Pro	Asn	Thr	Ile	Ser	Phe	Ser	Cys	Asn	Thr
	80					85						90			
Gly	Phe	Tyr	Leu	Asn	Gly	Ala	Asp	Ser	Ala	Lys	Cys	Thr	Glu	Glu	Gly
	95					100					105				
Lys	Trp	Ser	Pro	Glu	Leu	Pro	Val	Cys	Ala	Pro	Ile	Ile	Cys	Pro	Pro
110					115					120					125
Pro	Ser	Ile	Pro	Thr	Phe	Ala	Thr	Leu	Arg	Val	Tyr	Lys	Pro	Ser	Ala
				130					135					140	
Gly	Asn	Asn	Ser	Leu	Tyr	Arg	Asp	Thr	Ala	Val	Phe	Glu	Cys	Leu	Pro
			145					150					155		
Gln	His	Ala	Met	Phe	Gly	Asn	Asp	Thr	Ile	Thr	Cys	Thr	Thr	His	Gly
	160						165					170			
Asn	Trp	Thr	Lys	Leu	Pro	Glu	Cys	Arg	Glu	Val	Lys	Cys	Pro	Phe	Pro
	175					180					185				
Ser	Arg	Pro	Asp	Asn	Gly	Phe	Val	Asn	Tyr	Pro	Ala	Lys	Pro	Thr	Leu
190					195					200					205
Tyr	Tyr	Lys	Asp	Lys	Ala	Thr	Phe	Gly	Cys	His	Asp	Gly	Tyr	Ser	Leu
			210						215					220	
Asp	Gly	Pro	Glu	Glu	Ile	Glu	Cys	Thr	Lys	Leu	Gly	Asn	Trp	Ser	Ala
		225						230					235		
Met	Pro	Ser	Cys	Lys	Ala	Ser	Cys	Lys	Val	Pro	Val	Lys	Lys	Ala	Thr
		240					245					250			
Val	Val	Tyr	Gln	Gly	Glu	Arg	Val	Lys	Ile	Gln	Glu	Lys	Phe	Lys	Asn
	255					260					265				
Gly	Met	Leu	His	Gly	Asp	Lys	Val	Ser	Phe	Phe	Cys	Lys	Asn	Lys	Glu
270					275					280					285
Lys	Lys	Cys	Ser	Tyr	Thr	Glu	Asp	Ala	Gln	Cys	Ile	Asp	Gly	Thr	Ile
			290						295					300	
Glu	Val	Pro	Lys	Cys	Phe	Lys	Glu	His	Ser	Ser	Leu	Ala	Phe	Trp	Lys
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Thr	Asp	Ala	Ser	Asp	Val	Lys	Pro	Cys							
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<222> 1505..1520

<400> 107

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agc tcg aaa agc gat gcc gat tct ggt ttc ctg ggg ctg cgg ccc act      99
Ser Ser Lys Ser Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr
      15          20          25
tcg gtg gac cca gcg ctg agg cgg cgg cgg cga ggc cca aga aat aag      147
Ser Val Asp Pro Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys
      30          35          40
aag cgg ggc tgg cgg cgg ctt gct cag gag ccg ctg ggg ctg gag gtt      195
Lys Arg Gly Trp Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val
      45          50          55          60
gac cag ttc ctg gaa gac gtg cgg cta cag gag cgc acg agc ggt ggc      243
Asp Gln Phe Leu Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly
      65          70          75
ttg ttg tca gag gcc cca aat gaa aaa ctc ttc ttc gtg gac act ggc      291
Leu Leu Ser Glu Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly
      80          85          90
tcc aag gaa aaa ggg ctg aca aag aag aga acc aaa gtc cag aag aag      339
Ser Lys Glu Lys Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys
      95          100          105
tca ctg ctt ctc aag aaa ccc ctt cgg gtt gac ctc atc ctc gag aac      387
Ser Leu Leu Leu Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn
      110          115          120
aca tcc aaa gtc cct gcc ccc aaa gac gtc ctc gcc cac cag gtc ccc      435
Thr Ser Lys Val Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro
      125          130          135          140
aac gcc aag aag ctc agg cgg aag gag cag cta tgg gag aag ctg gcc      483
Asn Ala Lys Lys Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala
      145          150          155
aag cag ggc gag ctg ccc cgg gag gtg cgc agg gcc cag gcc cgg ctc      531
Lys Gln Gly Glu Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu
      160          165          170
ctc aac cct tct gca aca agg gcc aag ccc ggg ccc cag gac acc gta      579
Leu Asn Pro Ser Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val
      175          180          185
gag cgg ccc ttc tac gac ctc tgg gcc tca gac aac ccc ctg gac agg      627
Glu Arg Pro Phe Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg
      190          195          200
ccg ttg gtt ggc cag gat gag ttt ttc ctg gag cag acc aag aag aaa      675
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Pro	Leu	Val	Gly	Gln	Asp	Glu	Phe	Phe	Leu	Glu	Gln	Thr	Lys	Lys	Lys		
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Gly	Val	Lys	Arg	Pro	Ala	Arg	Leu	His	Thr	Lys	Pro	Ser	Gln	Ala	Pro		
				225					230					235			
gcc	gtg	gag	gtg	gcg	cct	gcc	gga	gct	tcc	tac	aat	cca	tcc	ttt	gaa	771	
Ala	Val	Glu	Val	Ala	Pro	Ala	Gly	Ala	Ser	Tyr	Asn	Pro	Ser	Phe	Glu		
			240					245					250				
gac	cac	cag	acc	ctg	ctc	tca	gcg	gcc	cac	gag	gtg	gag	ttg	cag	cgg	819	
Asp	His	Gln	Thr	Leu	Leu	Ser	Ala	Ala	His	Glu	Val	Glu	Leu	Gln	Arg		
		255					260					265					
cag	aag	gag	gcg	gag	aag	ctg	gag	cgg	cag	ctg	gcc	ctg	ccc	gcc	acg	867	
Gln	Lys	Glu	Ala	Glu	Lys	Leu	Glu	Arg	Gln	Leu	Ala	Leu	Pro	Ala	Thr		
	270				275				280								
gag	cag	gcc	gcc	acc	cag	gag	tcc	aca	ttc	cag	gag	ctg	tgc	gag	ggg	915	
Glu	Gln	Ala	Ala	Thr	Gln	Glu	Ser	Thr	Phe	Gln	Glu	Leu	Cys	Glu	Gly		
285					290				295					300			
ctg	ctg	gag	gag	tcg	gat	ggt	gag	ggg	gag	cca	ggc	cag	ggc	gag	ggg	963	
Leu	Leu	Glu	Glu	Ser	Asp	Gly	Glu	Gly	Glu	Pro	Gly	Gln	Gly	Glu	Gly		
				305				310						315			
ccg	gag	gct	ggg	gat	gcc	gag	gtc	tgt	ccc	acg	ccc	gcc	cgc	ctg	gcc	1011	
Pro	Glu	Ala	Gly	Asp	Ala	Glu	Val	Cys	Pro	Thr	Pro	Ala	Arg	Leu	Ala		
			320					325					330				
acc	aca	gag	aag	aag	acg	gag	cag	cag	cgg	cgg	cgg	gag	aag	gct	gtg	1059	
Thr	Thr	Glu	Lys	Lys	Thr	Glu	Gln	Arg	Arg	Arg	Arg	Glu	Lys	Ala	Val		
		335					340					345					
cac	agg	ctg	cgg	gta	cag	cag	gcc	gcg	ttg	cgg	gcc	gcc	cgg	ctc	cgg	1107	
His	Arg	Leu	Arg	Val	Gln	Gln	Ala	Ala	Leu	Arg	Ala	Ala	Arg	Leu	Arg		
	350					355			360								
cac	cag	gag	ctg	ttc	cgg	ctg	cgc	ggg	atc	aag	gcc	cag	gtg	gcc	ctg	1155	
His	Gln	Glu	Leu	Phe	Arg	Leu	Arg	Gly	Ile	Lys	Ala	Gln	Val	Ala	Leu		
365					370				375					380			
agg	ctg	gcg	gag	ctg	gcg	cgg	cgg	cag	agg	cgg	cgg	cag	gcg	cgg	cgg	1203	
Arg	Leu	Ala	Glu	Leu	Ala	Arg	Arg	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Arg		
				385				390					395				
gag	gct	gag	gct	gac	aag	ccc	cga	agg	ctg	ggg	cgg	ctc	aag	tac	cag	1251	
Glu	Ala	Glu	Ala	Asp	Lys	Pro	Arg	Arg	Leu	Gly	Arg	Leu	Lys	Tyr	Gln		
			400					405				410					
gca	cct	gac	atc	gac	gtg	cag	ctg	agc	tcg	gag	ctg	aca	gac	tcg	ctc	1299	
Ala	Pro	Asp	Ile	Asp	Val	Gln	Leu	Ser	Ser	Glu	Leu	Thr	Asp	Ser	Leu		
		415				420						425					
agg	acc	ctg	aag	ccc	gag	ggc	aac	atc	ctt	cga	gac	cgg	ttc	aag	agc	1347	
Arg	Thr	Leu	Lys	Pro	Glu	Gly	Asn	Ile	Leu	Arg	Asp	Arg	Phe	Lys	Ser		
	430					435					440						
ttc	cag	agg	agg	aat	atg	atc	gag	cct	cga	gag	aga	gcc	aag	ttc	aaa	1395	
Phe	Gln	Arg	Arg	Asn	Met	Ile	Glu	Pro	Arg	Glu	Arg	Ala	Lys	Phe	Lys		
445					450				455					460			
cgc	aag	tac	aag	gtg	aag	ctg	gtg	gag	aag	cgg	gcg	ttc	cgt	gag	atc	1443	
Arg	Lys	Tyr	Lys	Val	Lys	Leu	Val	Glu	Lys	Arg	Ala	Phe	Arg	Glu	Ile		
			465					470					475				
cag	ttg	tagctgccat	cagatgccgg	agactcgccc	ttcaataaaaa	aatctcttct										1499	
Gln	Leu																
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 <213> Homo sapiens

<400> 108

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Ala	Leu	Arg	Arg	Arg	Arg	Arg	Gly	Pro	Arg	Asn	Lys	Lys	Arg	Gly	Trp
	35						40					45			
Arg	Arg	Leu	Ala	Gln	Glu	Pro	Leu	Gly	Leu	Glu	Val	Asp	Gln	Phe	Leu
	50				55						60				
Glu	Asp	Val	Arg	Leu	Gln	Glu	Arg	Thr	Ser	Gly	Gly	Leu	Leu	Ser	Glu
65					70					75					80
Ala	Pro	Asn	Glu	Lys	Leu	Phe	Phe	Val	Asp	Thr	Gly	Ser	Lys	Glu	Lys
			85						90					95	
Gly	Leu	Thr	Lys	Lys	Arg	Thr	Lys	Val	Gln	Lys	Lys	Ser	Leu	Leu	Leu
		100						105					110		
Lys	Lys	Pro	Leu	Arg	Val	Asp	Leu	Ile	Leu	Glu	Asn	Thr	Ser	Lys	Val
		115					120					125			
Pro	Ala	Pro	Lys	Asp	Val	Leu	Ala	His	Gln	Val	Pro	Asn	Ala	Lys	Lys
	130					135						140			
Leu	Arg	Arg	Lys	Glu	Gln	Leu	Trp	Glu	Lys	Leu	Ala	Lys	Gln	Gly	Glu
145					150					155					160
Leu	Pro	Arg	Glu	Val	Arg	Arg	Ala	Gln	Ala	Arg	Leu	Leu	Asn	Pro	Ser
			165						170					175	
Ala	Thr	Arg	Ala	Lys	Pro	Gly	Pro	Gln	Asp	Thr	Val	Glu	Arg	Pro	Phe
		180						185					190		
Tyr	Asp	Leu	Trp	Ala	Ser	Asp	Asn	Pro	Leu	Asp	Arg	Pro	Leu	Val	Gly
	195						200					205			
Gln	Asp	Glu	Phe	Phe	Leu	Glu	Gln	Thr	Lys	Lys	Lys	Gly	Val	Lys	Arg
	210					215						220			
Pro	Ala	Arg	Leu	His	Thr	Lys	Pro	Ser	Gln	Ala	Pro	Ala	Val	Glu	Val
225					230					235					240
Ala	Pro	Ala	Gly	Ala	Ser	Tyr	Asn	Pro	Ser	Phe	Glu	Asp	His	Gln	Thr
			245						250					255	
Leu	Leu	Ser	Ala	Ala	His	Glu	Val	Glu	Leu	Gln	Arg	Gln	Lys	Glu	Ala
		260						265					270		
Glu	Lys	Leu	Glu	Arg	Gln	Leu	Ala	Leu	Pro	Ala	Thr	Glu	Gln	Ala	Ala
		275					280					285			
Thr	Gln	Glu	Ser	Thr	Phe	Gln	Glu	Leu	Cys	Glu	Gly	Leu	Leu	Glu	Glu
	290					295					300				
Ser	Asp	Gly	Glu	Gly	Glu	Pro	Gly	Gln	Gly	Glu	Gly	Pro	Glu	Ala	Gly
305					310					315					320
Asp	Ala	Glu	Val	Cys	Pro	Thr	Pro	Ala	Arg	Leu	Ala	Thr	Thr	Glu	Lys
			325						330					335	
Lys	Thr	Glu	Gln	Gln	Arg	Arg	Arg	Glu	Lys	Ala	Val	His	Arg	Leu	Arg
		340						345					350		
Val	Gln	Gln	Ala	Ala	Leu	Arg	Ala	Ala	Arg	Leu	Arg	His	Gln	Glu	Leu
	355						360					365			
Phe	Arg	Leu	Arg	Gly	Ile	Lys	Ala	Gln	Val	Ala	Leu	Arg	Leu	Ala	Glu
	370					375					380				
Leu	Ala	Arg	Arg	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Arg	Glu	Ala	Glu	Ala
385				390						395					400
Asp	Lys	Pro	Arg	Arg	Leu	Gly	Arg	Leu	Lys	Tyr	Gln	Ala	Pro	Asp	Ile
			405						410					415	
Asp	Val	Gln	Leu	Ser	Ser	Glu	Leu	Thr	Asp	Ser	Leu	Arg	Thr	Leu	Lys
		420						425					430		
Pro	Glu	Gly	Asn	Ile	Leu	Arg	Asp	Arg	Phe	Lys	Ser	Phe	Gln	Arg	Arg
	435						440						445		
Asn	Met	Ile	Glu	Pro	Arg	Glu	Arg	Ala	Lys	Phe	Lys	Arg	Lys	Tyr	Lys
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Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu
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 Met Cys Leu Leu Leu Ser Cys
 -10
 cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163
 Pro Cys His Pro Ser Ala His Gly Gln Ser Met Trp Ile Glu Arg Thr
 -5 1 5
 tcc ttc gtg act gca tac aag ctg ccg ggg atc ctg cgc tgg ttt gag 211
 Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu
 10 15 20 25
 gtg gtg cac atg tgc cag acc aca att agt cct ctg gag aat gcc ata 259
 Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile
 30 35 40
 gaa acc atg tcc acg gcc aat gag aag atc ctg atg atg ata aac cag 307
 Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu Met Met Ile Asn Gln
 45 50 55
 tac cag agt gat gag acc ctc ccc atc aac cca ctc tcc atg ctc ctg 355
 Tyr Gln Ser Asp Glu Thr Leu Pro Ile Asn Pro Leu Ser Met Leu Leu
 60 65 70
 aac ggg att gtg gac cct gct gtc atg gga ggc ttc gcc aag tat gag 403
 Asn Gly Ile Val Asp Pro Ala Val Met Gly Gly Phe Ala Lys Tyr Glu
 75 80 85
 aag gcc ttc ttc act gaa gag tat gtc agg gac cac cct gag gac cag 451
 Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg Asp His Pro Glu Asp Gln
 90 95 100 105
 gac aag ctg acc cac ctc aag gac ctg att gca tgg cag atc ccc ttc 499
 Asp Lys Leu Thr His Leu Lys Asp Leu Ile Ala Trp Gln Ile Pro Phe
 110 115 120
 ttg gga gct ggg att aag atc cat gag aaa agg gtg tca gat aac ttg 547
 Leu Gly Ala Gly Ile Lys Ile His Glu Lys Arg Val Ser Asp Asn Leu

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cga ccc ttc cat gac cgg atg gag gaa tgt ttc aag aac ctg aaa atg						595
Arg Pro Phe His Asp Arg Met Glu Glu Cys Phe Lys Asn Leu Lys Met						
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aag gtg gag aag gag tac ggt gtc cga gag atg cct gac ttt gac gac						643
Lys Val Glu Lys Glu Tyr Gly Val Arg Glu Met Pro Asp Phe Asp Asp						
	155		160		165	
agg aga gtg ggc cgt ccc agg tct atg ctg cgc tca tac aga cag atg						691
Arg Arg Val Gly Arg Pro Arg Ser Met Leu Arg Ser Tyr Arg Gln Met						
	170		175		180	185
tcc atc atc tct ctg gct tcc atg aat tct gac tgc agc acc ccc agc						739
Ser Ile Ile Ser Leu Ala Ser Met Asn Ser Asp Cys Ser Thr Pro Ser						
	190		195		200	
aag cct acc tca gag agc ttt gac ctg gaa tta gca tca ccc aag acg						787
Lys Pro Thr Ser Glu Ser Phe Asp Leu Glu Leu Ala Ser Pro Lys Thr						
	205		210		215	
ccg aga gtg gag cag gag gaa ccg atc tcc ccg ggg agc acc ctg cct						835
Pro Arg Val Glu Gln Glu Glu Pro Ile Ser Pro Gly Ser Thr Leu Pro						
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Glu Val Lys Leu Arg Arg Ser Lys Lys Arg Thr Lys Arg Ser Ser Val						
	235		240		245	
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Val Phe Ala Asp Glu Lys Ala Ala Ala Glu Ser Asp Leu Lys Arg Leu						
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tcc agg aag cat gag ttc atg agt gac acc aac ctc tcg gag cat gcg						979
Ser Arg Lys His Glu Phe Met Ser Asp Thr Asn Leu Ser Glu His Ala						
	270		275		280	
gcc atc ccc ctc aag gcg tct gtc ctc tct caa atg agc ttt gcc agc						1027
Ala Ile Pro Leu Lys Ala Ser Val Leu Ser Gln Met Ser Phe Ala Ser						
	285		290		295	
cag tcc atg cct acc atc cca gcc ctg gcg ctc tca gtg gca ggc atc						1075
Gln Ser Met Pro Thr Ile Pro Ala Leu Ala Leu Ser Val Ala Gly Ile						
	300		305		310	
cct ggg ttg gat gag gcc aac aca tct ccc cgc ctc agc cag acc ttc						1123
Pro Gly Leu Asp Glu Ala Asn Thr Ser Pro Arg Leu Ser Gln Thr Phe						
	315		320		325	
ctc caa ctc tca gat ggt gac aag aag aca ctc aca cgg aag aag gtc						1171
Leu Gln Leu Ser Asp Gly Asp Lys Lys Thr Leu Thr Arg Lys Lys Val						
	330		335		340	345
aat cag ttc ttc aag aca atg ctg gcc agc aaa tcg gct gaa gaa ggc						1219
Asn Gln Phe Phe Lys Thr Met Leu Ala Ser Lys Ser Ala Glu Glu Gly						
	350		355		360	
aaa cag atc cca gac tcg ctg tcc acg gac ctg tgagctgctg ctgactaggg						1272
Lys Gln Ile Pro Asp Ser Leu Ser Thr Asp Leu						
	365		370			
ctgcatggga gagccagga ggggagtttc tggaagagga aagccatgcg tggaacatcg						1332
aagcctcaga gagtgggaga ctgtcccat cagttgtcct tacttagagg agacagagag						1392
gccaatcagg tcccagagct tgaatgctaa caagcccagc atcccctggg gctgtgatca						1452
tggtggatga ggaagcctca acgtagattc ctgaactcaa ggtaccagca agaatgcctt						1512
ctcccagtggt gctctcccca acatcctagg cacagctttc ataaccaggt ttcttaggtg						1572
taagaaaactg tttttatctc atttattaag tctcagaact taacagaaaa ggaagccttt						1632
taaatattct ttttaatttt atttttagatt aacagttttg tactttacat ttttttatac						1692
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<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..15

<400> 110

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		5						10					15		
Gly	Ile	Leu	Arg	Trp	Phe	Glu	Val	Val	His	Met	Ser	Gln	Thr	Thr	Ile
	20					25						30			
Ser	Pro	Leu	Glu	Asn	Ala	Ile	Glu	Thr	Met	Ser	Thr	Ala	Asn	Glu	Lys
	35					40					45				
Ile	Leu	Met	Met	Ile	Asn	Gln	Tyr	Gln	Ser	Asp	Glu	Thr	Leu	Pro	Ile
50					55					60					65
Asn	Pro	Leu	Ser	Met	Leu	Leu	Asn	Gly	Ile	Val	Asp	Pro	Ala	Val	Met
				70					75					80	
Gly	Gly	Phe	Ala	Lys	Tyr	Glu	Lys	Ala	Phe	Phe	Thr	Glu	Glu	Tyr	Val
		85						90					95		
Arg	Asp	His	Pro	Glu	Asp	Gln	Asp	Lys	Leu	Thr	His	Leu	Lys	Asp	Leu
	100						105					110			
Ile	Ala	Trp	Gln	Ile	Pro	Phe	Leu	Gly	Ala	Gly	Ile	Lys	Ile	His	Glu
	115					120					125				
Lys	Arg	Val	Ser	Asp	Asn	Leu	Arg	Pro	Phe	His	Asp	Arg	Met	Glu	Glu
130					135					140				145	
Cys	Phe	Lys	Asn	Leu	Lys	Met	Lys	Val	Glu	Lys	Glu	Tyr	Gly	Val	Arg
			150						155					160	
Glu	Met	Pro	Asp	Phe	Asp	Asp	Arg	Arg	Val	Gly	Arg	Pro	Arg	Ser	Met
			165					170					175		
Leu	Arg	Ser	Tyr	Arg	Gln	Met	Ser	Ile	Ile	Ser	Leu	Ala	Ser	Met	Asn
	180						185					190			
Ser	Asp	Cys	Ser	Thr	Pro	Ser	Lys	Pro	Thr	Ser	Glu	Ser	Phe	Asp	Leu
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Glu	Leu	Ala	Ser	Pro	Lys	Thr	Pro	Arg	Val	Glu	Gln	Glu	Glu	Pro	Ile
210					215					220				225	
Ser	Pro	Gly	Ser	Thr	Leu	Pro	Glu	Val	Lys	Leu	Arg	Arg	Ser	Lys	Lys
			230						235					240	
Arg	Thr	Lys	Arg	Ser	Ser	Val	Val	Phe	Ala	Asp	Glu	Lys	Ala	Ala	Ala
		245						250					255		
Glu	Ser	Asp	Leu	Lys	Arg	Leu	Ser	Arg	Lys	His	Glu	Phe	Met	Ser	Asp
	260					265					270				
Thr	Asn	Leu	Ser	Glu	His	Ala	Ala	Ile	Pro	Leu	Lys	Ala	Ser	Val	Leu
	275					280					285				
Ser	Gln	Met	Ser	Phe	Ala	Ser	Gln	Ser	Met	Pro	Thr	Ile	Pro	Ala	Leu
290					295					300				305	
Ala	Leu	Ser	Val	Ala	Gly	Ile	Pro	Gly	Leu	Asp	Glu	Ala	Asn	Thr	Ser
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Pro	Arg	Leu	Ser	Gln	Thr	Phe	Leu	Gln	Leu	Ser	Asp	Gly	Asp	Lys	Lys
			325					330					335		
Thr	Leu	Thr	Arg	Lys	Lys	Val	Asn	Gln	Phe	Phe	Lys	Thr	Met	Leu	Ala
	340						345					350			
Ser	Lys	Ser	Ala	Glu	Glu	Gly	Lys	Gln	Ile	Pro	Asp	Ser	Leu	Ser	Thr
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 Met Ser Thr Phe
 1
 ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162
 Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys
 5 10 15 20
 ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc 210
 Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser
 25 30 35
 tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258
 Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu
 40 45 50
 tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306
 Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met
 55 60 65
 tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354
 Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala
 70 75 80
 gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402
 Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys
 85 90 95 100
 tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa 450
 Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu
 105 110 115
 aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc 498
 Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu
 120 125 130
 tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct 546
 Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala
 135 140 145
 tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594
 Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val
 150 155 160

atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt	642
Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu	
165 170 175 180	
ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act	690
Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn Phe Phe Gly Thr	
185 190 195	
gtg gag gtc aca aag acg ttt ttg cct ctt aga aaa tcc aaa ggg	738
Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly	
200 205 210	
agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtg gaa agg	786
Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg	
215 220 225	
ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca	834
Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser	
230 235 240	
gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc	882
Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile	
245 250 255 260	
caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg	930
Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp	
265 270 275	
gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag	978
Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln	
280 285 290	
gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta	1026
Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg Asn Phe Leu Leu	
295 300 305	
ttg atc aac tcg tta gcc agc aag gac ttc tct ccg gtg ctg cgg gac	1074
Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro Val Leu Arg Asp	
310 315 320	
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Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala Tyr Tyr Thr Pro	
325 330 335 340	
ggg aaa ggc gct tac ttg tgg atc tgc ctt gct cac tat ttg cct att	1170
Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His Tyr Leu Pro Ile	
345 350 355	
ggc ata tat gat tac ttt gct aaa aga cat ttt ggc caa gac aag ccc	1218
Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly Gln Asp Lys Pro	
360 365 370	
atg ccc aga gct tta aga atg cct aac tac aag aaa aag gcc ccc	1263
Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys Lys Ala Pro	
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<212> PRT

<213> Homo sapiens

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35 40 45	
Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser	

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Cys	Phe	Leu	Met	Tyr	Thr	Tyr	Leu	Ser	Gly	Gln	Glu	Leu	Leu	Pro	Val	
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Asp	Gln	Lys	Ala	Val	Leu	Val	Thr	Gly	Gly	Asp	Cys	Gly	Leu	Gly	His	
				85					90					95		
Ala	Leu	Cys	Lys	Tyr	Leu	Asp	Glu	Leu	Gly	Phe	Thr	Val	Phe	Ala	Gly	
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Val	Leu	Asn	Glu	Asn	Gly	Pro	Gly	Ala	Glu	Glu	Leu	Arg	Arg	Thr	Cys	
		115					120					125				
Ser	Pro	Arg	Leu	Ser	Val	Leu	Gln	Met	Asp	Ile	Thr	Lys	Pro	Val	Gln	
	130					135					140					
Ile	Lys	Asp	Ala	Tyr	Ser	Lys	Val	Ala	Ala	Met	Leu	Gln	Asp	Arg	Gly	
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Leu	Trp	Ala	Val	Ile	Asn	Asn	Ala	Gly	Val	Leu	Gly	Phe	Pro	Thr	Asp	
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Gly	Glu	Leu	Leu	Leu	Met	Thr	Asp	Tyr	Lys	Gln	Cys	Met	Ala	Val	Asn	
		180						185					190			
Phe	Phe	Gly	Thr	Val	Glu	Val	Thr	Lys	Thr	Phe	Leu	Pro	Leu	Leu	Arg	
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Lys	Ser	Lys	Gly	Arg	Leu	Val	Asn	Val	Ser	Ser	Met	Gly	Gly	Gly	Ala	
	210					215					220					
Pro	Val	Glu	Arg	Leu	Ala	Ser	Tyr	Gly	Ser	Ser	Lys	Ala	Ala	Val	Thr	
225					230						235				240	
Met	Phe	Ser	Ser	Val	Met	Arg	Leu	Glu	Leu	Ser	Lys	Trp	Gly	Ile	Lys	
			245						250					255		
Val	Ala	Ser	Ile	Gln	Pro	Gly	Gly	Phe	Leu	Thr	Asn	Ile	Ala	Gly	Thr	
		260					265						270			
Ser	Asp	Lys	Trp	Glu	Lys	Leu	Glu	Lys	Asp	Ile	Leu	Asp	His	Leu	Pro	
	275						280					285				
Ala	Glu	Val	Gln	Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg	
	290					295					300					
Asn	Phe	Leu	Leu	Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro	
305					310						315				320	
Val	Leu	Arg	Asp	Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala	
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Tyr	Tyr	Thr	Pro	Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His	
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Tyr	Leu	Pro	Ile	Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly	
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Gln	Asp	Lys	Pro	Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys	
	370					375					380					
Lys	Ala	Pro														
385																